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SEARCH REQUEST FORM

Scientific and Technical Information Center

Access DB# 49081

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

Searcher: Al Zhou - Early
Searcher Phone #: 308-4501
Searcher Location: Buried Lab
Date Searcher Picked Up: 8/16/01
Date Completed: 8/17/01
Searcher Prep & Review Time: _____
Clerical Prep Time: 4m
Online Time: 2m

Type of Search

NA Sequence (#) _____
AA Sequence (#) 1
Structure (#) _____
Bibliographic _____
Litigation _____
Fulltext _____
Patent Family _____
Other _____

Vendors and cost where applicable

STN _____
Dialog _____
Questel/Orbit _____
Dr. Link _____
Lexis/Nexis _____
Sequence Systems ABSS02
WWW/Internet _____
Other (specify) _____

49081

From: Chan, Christina
Sent: Thursday, August 16, 2001 11:09 AM
To: Huff, Sheela; STIC-Biotech/ChemLib
Subject: RE: RUSh sequence search for 09/428082

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE, 1644
CM 1, Room 9B19
308-3973

CRF6

-----Original Message-----

From: Huff, Sheela
Sent: Thursday, August 16, 2001 9:07 AM
To: Chan, Christina
Subject: RUSh sequence search for 09/428082

Christina--can you please approve this search??

Please search and interference search SEQ ID No. 213 of 09/428082.

Thanks

Sheela Huff
Art Unit 1642
8B07
305-7866

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 16, 2001, 14:54:14 ; Search time 10.52 Seconds
(without alignments)
33.929 Million cell updates/sec

Title: US-09-428-082-213
Perfect score: 124
Sequence: 1 TANSSFEWTPYWPYALPL 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

rchched: 115903 seqs, 16996782 residues

Total number of hits satisfying chosen parameters: 115903

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_New: *
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep: *
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep: *
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep: *
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep: *
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep: *
6: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 67.5 | 54.4 | 22 | 5 | US-09-880-132-58 |
| 2 | 67.5 | 54.4 | 22 | 5 | US-09-880-149-58 |
| 3 | 56 | 45.2 | 12 | 5 | US-09-880-132-59 |
| 4 | 56 | 45.2 | 12 | 5 | US-09-880-149-59 |
| 5 | 50 | 40.3 | 549 | 5 | US-09-803-110-9106 |
| 6 | 44 | 35.5 | 322 | 1 | PCT-US01-08656-6632 |
| 7 | 44 | 35.5 | 336 | 5 | US-09-803-110-8965 |
| 8 | 43 | 34.7 | 138 | 1 | PCT-US01-08656-5771 |
| 9 | 43 | 34.7 | 194 | 5 | US-09-758-466-6330 |
| 10 | 43 | 34.7 | 272 | 5 | US-09-803-110-8377 |
| 11 | 43 | 34.7 | 467 | 5 | US-09-664-6108-195 |
| 12 | 42 | 33.9 | 127 | 5 | US-09-758-470-402 |
| 13 | 42 | 33.9 | 137 | 5 | US-09-758-475-366 |
| 14 | 42 | 33.9 | 144 | 1 | PCT-US01-16450-2224 |
| 15 | 42 | 33.9 | 168 | 5 | US-09-758-463-977 |
| 16 | 41.5 | 33.5 | 495 | 5 | US-09-803-110-11517 |
| 17 | 41 | 33.1 | 230 | 5 | US-09-760-455-51 |
| 18 | 41 | 33.1 | 270 | 5 | US-09-803-110-12437 |
| 19 | 41 | 33.1 | 385 | 5 | US-09-738-626-4559 |
| 20 | 41 | 33.1 | 503 | 5 | US-09-738-626-5485 |
| 21 | 41 | 33.1 | 684 | 5 | US-09-760-469-1228 |
| 22 | 40.5 | 32.7 | 109 | 5 | US-09-694-951B-8 |
| 23 | 40.5 | 32.7 | 204 | 5 | US-09-758-445-503 |
| 24 | 40 | 32.3 | 58 | 5 | US-09-758-474-784 |
| 25 | 40 | 32.3 | 58 | 5 | US-09-758-466-521 |
| 26 | 40 | 32.3 | 63 | 1 | PCT-US01-18569-3799 |
| 27 | 40 | 32.3 | 159 | 5 | US-09-760-469-1249 |

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28 40 32.3 183 5 US-09-738-626-5595 Sequence 5595, Ap
29 40 32.3 205 5 US-09-602-787A-648 Sequence 648, Ap
30 40 32.3 255 1 PCT-US01-18569-3054 Sequence 3054, Ap
31 40 32.3 273 5 US-09-760-469-1716 Sequence 1716, Ap
32 40 32.3 273 5 US-09-738-626-5643 Sequence 5643, Ap
33 40 32.3 374 5 US-09-738-626-6901 Sequence 6901, Ap
34 40 32.3 425 1 PCT-US01-20592-25 Sequence 25, Appl
35 40 32.3 466 1 PCT-US01-18569-2789 Sequence 2789, Appl
36 40 32.3 466 5 US-09-758-471-4338 Sequence 4338, Ap
37 39.5 31.9 880 1 PCT-US01-20592-36 Sequence 36, Appl
38 39 31.5 99 5 US-09-758-472-5177 Sequence 5177, Ap
39 39 31.5 112 5 US-09-760-479-760 Sequence 760, Ap
40 39 31.5 133 5 US-09-758-473-1010 Sequence 1010, Ap
41 39 31.5 206 1 PCT-US01-14827-15804 Sequence 15804, A
42 39 31.5 315 5 US-09-602-787A-454 Sequence 454, App
43 39 31.5 330 1 PCT-US01-16450-2183 Sequence 2183, Ap
44 39 31.5 484 5 US-09-602-787A-452 Sequence 452, App
45 39 31.5 521 1 PCT-US01-18569-2799 Sequence 2799, Ap

```

ALIGNMENTS

```

RESULT 1
US-09-880-132-58
; Sequence 58, Application US/09880132
; GENERAL INFORMATION:
; APPLICANT: Kenten, John
; APPLICANT: Roberts, Steven
; TITLE OF INVENTION: CONTROLLING PROTEIN LEVELS IN EUKARYOTIC ORGANISMS
; FILE REFERENCE: 2757-6
; CURRENT APPLICATION NUMBER: US/09/880,132
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/406,781
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 60/119,851
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: binding peptide
US-09-880-132-58

```

```

Query Match 54.4%; Score 67.5; DB 5; Length 22;
Best Local Similarity 63.2%; Pred. No. 0.00083;
Matches 12; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

```

```

Qy 6 SFEW---TPYWPYALPL 21
   :| | | | | | | | | |
Db 4 TFTWEESNAYWPYALPL 22

```

```

RESULT 2
US-09-880-149-58
; Sequence 58, Application US/09880149
; GENERAL INFORMATION:
; APPLICANT: Kenten, John
; APPLICANT: Roberts, Steven
; TITLE OF INVENTION: CONTROLLING PROTEIN LEVELS IN EUKARYOTIC ORGANISMS
; FILE REFERENCE: 2757-5
; CURRENT APPLICATION NUMBER: US/09/880,149
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/406,781
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 60/119,851
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1

```

; SEQ ID NO 58
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: binding peptide
US-09-880-149-58

Query Match 54.4%; Score 67.5; DB 5; Length 22;
Best Local Similarity 63.2%; Pred. No. 0.00083;
Matches 12; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

QY 6 SPEW---TPYYWQPYALPL 21
: | | | | | | | | | |
Db 4 TPTWESNAYWQPYALPL 22

RESULT 3
US-09-880-132-59
; Sequence 59, Application US/09880132
; GENERAL INFORMATION:
; APPLICANT: Kenten, John
; TITLE OF INVENTION: CONTROLLING PROTEIN LEVELS IN EUKARYOTIC ORGANISMS
; FILE REFERENCE: 2757-6
; CURRENT APPLICATION NUMBER: US/09/880,132
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/406,781
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: 60/119,851
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: binding peptide
US-09-880-132-59

Query Match 45.2%; Score 56; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 YWQPYALPL 21
: | | | | | | | | | |
Db 4 YWQPYALPL 12

RESULT 4
US-09-880-149-59
; Sequence 59, Application US/09880149
; GENERAL INFORMATION:
; APPLICANT: Kenten, John
; TITLE OF INVENTION: CONTROLLING PROTEIN LEVELS IN EUKARYOTIC ORGANISMS
; FILE REFERENCE: 2757-5
; CURRENT APPLICATION NUMBER: US/09/880,149
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/406,781
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: 60/119,851
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: binding peptide
US-09-880-149-59

Query Match 45.2%; Score 56; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 YWQPYALPL 21
: | | | | | | | | | |
Db 4 YWQPYALPL 12

RESULT 5
US-09-803-110-9106
; Sequence 9106, Application US/09803110
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)D
; CURRENT APPLICATION NUMBER: US/09/803,110
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/739,449
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: US 60/168,139
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 9106
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-803-110-9106

Query Match 40.3%; Score 50; DB 5; Length 549;
Best Local Similarity 44.4%; Pred. No. 6.6;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 TANVSSEFWTPYYWQPYA 18
: | | | | | | | | | |
Db 301 TKPVSLYSWLPFWQGV 318

RESULT 6
PCT-US01-08656-6632
; Sequence 6632, Application PC/TUS0108656
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: PCT/US01/08656
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 6632
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-08656-6632

Query Match 35.5%; Score 44; DB 1; Length 322;
Best Local Similarity 63.6%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 WTPYYWQPYAL 19

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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM036
; CURRENT APPLICATION NUMBER: US/09/758,466
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 814
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 630
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (17)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (22)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-758-466-630

```

```

Query Match 35.5%; Score 44; DB 5; Length 336;
Best Local Similarity 54.5%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY 9 WTPYWPQYALP 19
| | | | |
Db 210 WLGYNWSPAT 220

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```

RESULT 8
PCT-US01-08656-5771
; Sequence 5771, Application PC/TUS0108656
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: PCT/US01/08656
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 5771
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-08656-5771

```

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Query Match 34.7%; Score 43; DB 1; Length 138;
Best Local Similarity 46.7%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

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QY 6 SFWTYPYWPQYALP 20
| | | | |
Db 64 SSPMPVTFWFGLP 78

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RESULT 9
US-09-758-466-630
; Sequence 630, Application US/09758466
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM036
; CURRENT APPLICATION NUMBER: US/09/758,466
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 814
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 630
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (17)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (22)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-758-466-630

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Query Match 34.7%; Score 43; DB 5; Length 194;
Best Local Similarity 44.4%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

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QY 3 NVSSFETPYWPQYALP 20
| | | | |
Db 138 NEPSNDWDIYWATEAKP 155

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RESULT 10
US-09-803-110-8377
; Sequence 8377, Application US/09803110
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)D
; CURRENT APPLICATION NUMBER: US/09/803,110
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/739,449
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: US 60/168,139
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 8377
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-803-110-8377

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```

Query Match 34.7%; Score 43; DB 5; Length 272;
Best Local Similarity 54.5%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY 9 WTPYWPQYALP 19
| | | | |
Db 146 WVGYYWAPTSL 156

```

```

RESULT 11
US-09-664-610B-195
; Sequence 195, Application US/09664610B
; GENERAL INFORMATION:

```

APPLICANT: CHEN, JIAN
APPLICANT: GODDARD, AUDREY
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: HILLAN, KENNETH
APPLICANT: PENNICCA, DIANE
APPLICANT: WOOD, WILLIAM T.
APPLICANT: YUAN, JEAN
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIC
FILE REFERENCE: 10466/13
CURRENT APPLICATION NUMBER: US/09/664,610B
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: 1998-09-16
NUMBER OF SEQ ID NOS: 379
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 195
LENGTH: 467
TYPE: PRT
ORGANISM: Homo sapiens
9-664-610B-195

Query Match 34.7%; Score 43; DB 5; Length 467;
Best Local Similarity 45.0%; Pred. No. 56;
Matches 9; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 3 NVSSF--EWTPYWPYALP 20
Db 65 SVPFGEFWFYWQKXIP 84

RESULT 12
US-09-758-470-402
Sequence 402, Application US/09758470
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PN030
CURRENT APPLICATION NUMBER: US/09/758,470
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 722
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 402
LENGTH: 127
TYPE: PRT
ORGANISM: Homo sapiens
US-09-758-470-402

Query Match 33.9%; Score 42; DB 5; Length 127;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 9 WTPYWPY 18
Db 25 WRPWWKPR 34

RESULT 13
US-09-758-475-366
Sequence 366, Application US/09758475
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PM035
CURRENT APPLICATION NUMBER: US/09/758,475

CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 466
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 366
LENGTH: 137
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (17)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-475-366

Query Match 33.9%; Score 42; DB 5; Length 137;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 7; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 TANVSSFETPPYWPYALPL 21
Db 86 TVNVVPFVWTSFFRAQYVP 106

RESULT 14
PCT-US01-16450-2224
Sequence 2224, Application PC/TUS0116450
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA131PCT
CURRENT APPLICATION NUMBER: PCT/US01/16450
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2820
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2224
LENGTH: 144
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (89)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (131)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-16450-2224

Query Match 33.9%; Score 42; DB 1; Length 144;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 WTPYWP 14
Db 135 WQPYWP 140

RESULT 15
US-09-758-463-977
Sequence 977, Application US/09758463
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PM011
CURRENT APPLICATION NUMBER: US/09/758,463
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065

;; PRIOR FILING DATE: 2000-01-31
;; PRIOR APPLICATION NUMBER: 60/180,628
;; PRIOR FILING DATE: 2000-02-04
;; NUMBER OF SEQ ID NOS: 1304
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 977
;; LENGTH: 168
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (48)
;; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (144)
;; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-758-463-977

Query Match 33.9%; Score 42; DB 5; Length 168;
Best Local Similarity 46.7%; Pred. No. 28;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 7 FEWTPYVQPYALPL 21
DB 134 YEWCPSPHPXLLPL 148

Search completed: August 16, 2001, 14:57:10
Job time: 176 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 16, 2001, 14:53:49 ; Search time 12.82 Seconds
(without alignments)
124.779 Million cell updates/sec

Title: US-09-428-082-213

Perfect score: 124

Sequence: 1 TANVSSFEWTPYWPYALPL 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 48 | 38.7 | 525 | 2 T08027 | glucose-1-phosphat |
| 2 | 47.5 | 38.3 | 109 | 2 H85583 | probable tail comp |
| 3 | 46.5 | 37.5 | 201 | 2 T16878 | hypothetical prote |
| 4 | 46 | 37.1 | 856 | 2 T00349 | Avicelase III - As |
| 5 | 46 | 37.1 | 1193 | 2 JC2489 | peptidyl-dipeptida |
| 6 | 45 | 36.3 | 132 | 2 S03480 | T-cell receptor al |
| 7 | 45 | 36.3 | 344 | 2 T27119 | hypothetical prote |
| 8 | 45 | 36.3 | 509 | 2 T03275 | probable cytochrom |
| 9 | 44 | 35.5 | 139 | 1 RKAUS | ribulose-bisphosph |
| 10 | 44 | 35.5 | 139 | 1 RKPSL | ribulose-bisphosph |
| 11 | 44 | 35.5 | 161 | 2 E70530 | hypothetical prote |
| 12 | 44 | 35.5 | 254 | 2 T01109 | hypothetical prote |
| 13 | 44 | 35.5 | 301 | 2 T40593 | cytoplasmic dynein |
| 14 | 44 | 35.5 | 314 | 1 S48466 | MOB1 protein [vali |
| 15 | 44 | 35.5 | 334 | 2 T25055 | hypothetical prote |
| 16 | 44 | 35.5 | 401 | 2 S65138 | glucoprotein anti |
| 17 | 44 | 35.5 | 420 | 1 JN0854 | glutamate dehydrog |
| 18 | 44 | 35.5 | 420 | 2 A74110 | glutamate dehydrog |
| 19 | 44 | 35.5 | 420 | 2 D75176 | glutamate dehydrog |
| 20 | 44 | 35.5 | 422 | 2 A71038 | probable glutamate |
| 21 | 44 | 35.5 | 427 | 2 S74211 | PAS-6/7 protein pr |
| 22 | 44 | 35.5 | 632 | 2 B69310 | mRNA 3'-end proces |
| 23 | 44 | 35.5 | 720 | 2 T02734 | hypothetical prote |
| 24 | 44 | 35.5 | 772 | 2 E86042 | hypothetical prote |
| 25 | 44 | 35.5 | 772 | 2 B65167 | hypothetical 88.1 |
| 26 | 44 | 35.5 | 955 | 2 T39765 | probable nuclear m |
| 27 | 43.5 | 35.1 | 283 | 2 S44848 | K06H7.8 protein - |
| 28 | 43.5 | 35.1 | 644 | 2 H75141 | oligopeptide-bind |
| 29 | 43 | 34.7 | 61 | 2 S51240 | puc4A protein - Rh |

30 43 34.7 198 2 F70853
31 43 34.7 297 2 A45442
32 43 34.7 342 1 C69395
33 43 34.7 354 2 S75877
34 43 34.7 434 2 S77607
35 43 34.7 437 2 T37469
36 43 34.7 449 2 T19626
37 43 34.7 521 2 C85862
38 43 34.7 529 2 T39841
39 43 34.7 531 1 S54098
40 43 34.7 533 2 T19416
41 43 34.7 624 2 T38006
42 43 34.7 624 2 T20445
43 43 34.7 3036 2 T18995
44 43 34.7 4351 2 T00252
45 42.5 34.3 159 2 S07372

probable leuD prot
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hypothetical prote
glutamate/glutamin
homogentisate 1,2-
hypothetical prote
hypothetical prote
transcription regu
1-phosphatidylinos
hypothetical prote
probable lysophosp
hypothetical prote
hypothetical prote
MEGFI protein - ra
hypothetical prote

ALIGNMENTS

RESULT 1

T08027

glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) large chain - Oriental melon
N:Alternate names: ADP-glucose pyrophosphorylase large chain
C:Species: Cucumis melo var. markuwa Markino (Oriental melon)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
C:Accession: T08027
R:Park, S.W.; Kahng, H.Y.; Park, J.O.; Kim, I.J.; Chung, W.I.
submitted to the EMBL Data Library, October 1997

A:Description: Molecular cloning of ADP-glucose pyrophosphorylase small and large sub
A:Reference number: Z16300
A:Accession: T08027
A>Status: translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-525 <PAR>

A:Cross-references: EMBL:AF030383; NID:g2625085; PID:g2625086

A:Experimental source: cv. Euncheon

C:Genetics:

A:Gene: mlf1

C:Function:

A:Description: catalyzes the formation of ADPglucose and pyrophosphate from alpha-D-g
A:Pathway: glycogen/starch biosynthesis (ADPglucose-utilizing)

C:Superfamily: glucose-1-phosphate adenylyltransferase

C:Keywords: nucleotidyltransferase

Query Match 38.7%; Score 48; DB 2; Length 525;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 11; Conservative 2; Mismatches 5; Indels 4; Gaps 1;

QY 3 NVSSFEW---TPYWPYALP 20

Db 372 NVSRFEYDPKTPFTSPRFLP 393

RESULT 2

H85583

probable tail component of prophage CP-933K 20976 [imported] - Escherichia coli (stra
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
Nature 409, 529-533, 2001

C:Accession: H85583

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: H85583

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-109 <STO>

A:Cross-references: GB:AE005174; NID:g12513744; PIDN:AAG55132.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z0976
C:Superfamily: phage lambda minor tail protein M

Query Match 38.3%; Score 47.5; DB 2; Length 109;
Best Local Similarity 57.1%; Pred. No. 6.3;
Matches 8; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 4 VSSFWEPT-PYWPQ 16

Db 58 VRAFQWTPPYDKP 81

RESULT 3

hypothetical protein T14G12.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 15-Sep-2000

C:Accession: T16878

R:Wilcox, L.

Submitted to the EMBL Data Library, November 1995

Description: The sequence of C. elegans cosmid T14G12.

Reference number: Z18596

C:Accession: T16878

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-201 <WIL>

A:Cross-references: EMBL:U01268; NID:g1086843; PID:g1086845; PIDN:AAA82434.1; CESP-T14G12

C:Genetics:

A:Gene: CESP-T14G12.3

A:Introns: 32/2; 61/3; 144/2; 189/1

C:Superfamily: Caenorhabditis elegans hypothetical protein R13H4.2

Query Match

37.5%; Score 46.5; DB 2; Length 201;

Best Local Similarity 41.2%; Pred. No. 16;

Matches 7; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Qy 2 ANVSFE-WTPYWPQY 17

Db 65 SNIDRYTFYWPYQTY 81

RESULT 4

T00349

Avicelase III - Aspergillus aculeatus

C:Species: Aspergillus aculeatus

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Jul-1999

C:Accession: T00349

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-856 <ARA>

A:Cross-references: EMBL:AB015511; NID:d1199887; PID:d1029971

C:Genetics:

A:Gene: avIII

C:Superfamily: fungal cellulose-binding domain homology

F:823-854/Domain: fungal cellulose-binding domain homology <FCB>

Query Match

37.1%; Score 46; DB 2; Length 856;

Best Local Similarity 57.1%; Pred. No. 85;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ANVSFEWTPYWPQ 15

Db 182 SNVTSFTWTGTYFQ 195

RESULT 5

JC2489

peptidyl-dipeptidase A (EC 3.4.15.1) - chicken

N:Alternate names: angiotensin converting enzyme

C:Species: Gallus gallus (chicken)

C>Date: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 28-May-1999

C:Accession: JC2489

R:Esther, C.R.; Thomas Jr., K.E.; Bernstein, K.E.

Biochem. Biophys. Res. Commun. 205, 1916-1921, 1994

A:Title: Chicken lacks the testis specific isozyme of angiotensin converting enzyme f

A:Reference number: JC2489; MUID:95110342

A:Accession: JC2489

A:Molecule type: mRNA

A:Residues: 1-1193 <EST>

A:Cross-references: GB:L40175; NID:g685168; PIDN:AAA75554.1; PID:g994708

C:Comment: This enzyme is a zinc dependant dipeptidyl carboxypeptidase that cleaves a

C:Superfamily: mammalian peptidyl-dipeptidase A

C:Keywords: metal binding; peptidyl-dipeptide hydrolase; zinc

F:316.331,914,929/Binding site: zinc, catalytic (Glu, His, Glu, His) #status predicted

Query Match

37.1%; Score 46; DB 2; Length 1193;

Best Local Similarity 42.1%; Pred. No. 1.2e+02;

Matches 8; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TANVSFEWTPYWPQYAL 19

Db 1111 TENGEVLGWPEYSWTPYAV 1129

RESULT 6

S03480

T-cell receptor alpha chain precursor V-J region (TA39) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999

C:Accession: S03480

R:Arden, B.; Klotz, J.L.; Siu, G.; Hood, L.E.

Nature 316, 783-787, 1985

A:Title: Diversity and structure of genes of the alpha family of mouse T-cell antigen

A:Reference number: S03467; MUID:85296324

A:Accession: S03480

A:Molecule type: mRNA

A:Residues: 1-132 <ARD>

A:Cross-references: EMBL: X02929; NID:g54411; PIDN:CAA26684.1; PID:g54412

A>Note: this sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

F:1-132/Product: T-cell receptor alpha chain (fragment) #status predicted <MAT>

F:1-20/Domain: signal sequence (fragment) #status predicted <SIG>

F:21-112/Domain: V region (TA39) #status predicted <VRE>

F:114-130/Domain: J region #status predicted <JRE>

Query Match

36.3%; Score 45; DB 2; Length 132;

Best Local Similarity 54.5%; Pred. No. 17;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SSFEWTPYWPQ 15

Db 47 STFDYFPYWPQ 57

RESULT 7

T27119

hypothetical protein Y53C10A.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000

C:Accession: T27119

R:White, S.

submitted to the EMBL Data Library, November 1998

A:Reference number: Z20314

A:Accession: T27119

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-344 <WIL>

A:Cross-references: EMBL:AL033536; PIDN:CAA22140.1; CESP:Y53C10A.6

A:Experimental source: clone Y53C10A

C:Genetics:

A:Gene: CESP:Y53C10A.6

A:Introns: 20/2; 33/1; 61/3; 113/1; 167/3; 233/3; 313/1

C:Superfamily: Caenorhabditis elegans hypothetical protein Y53C10A.6

Query Match 36.3%; Score 45; DB 2; Length 344;

Best Local Similarity 47.6%; Pred. No. 46;

Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 TANVSSFETPPYQPYALPL 21

||||:||||:||||:

123 TANVOAFELPNPKPATRL 143

RESULT 8

T03275

probable cytochrome P450, hypersensitivity-related - common tobacco

N:Alternate names: protein hsr515

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 28-Jul-2000

C:Accession: T03275

R:Czernic, P.; Huang, H.C.; Marco, Y.

Plant Mol. Biol. 31, 255-265, 1996

A:Title: Characterization of hsr201 and hsr515, two tobacco genes preferentially expressed

A:Reference number: Z14876; MUID:96343929

A:Accession: T03275

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-509 <CZE>

A:Cross-references: EMBL:X95342; NID:g1171578; PIDN:CAA64635.1; PID:g1171579

A:Experimental source: cultivar bottom special; tissue-type leaf

C:Genetics:

A:Gene: hsr515

C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase

F:302-466/Domain: cytochrome P450 homology <P45>

F:444/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 36.3%; Score 45; DB 2; Length 509;

Best Local Similarity 47.1%; Pred. No. 69;

Matches 8; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 TANVSSFETPPY--YQW 15

||||:||||:||||:

Db 110 TYNYSITWSPYGPYWR 126

RESULT 9

RKAUS

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain - brown alga (Ectocarpus sil

C:Species: Chloroplast Ectocarpus siliculosus

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1999

C:Accession: S13124

R:Valentin, K.; Zetsche, K.

Plant Mol. Biol. 15, 575-584, 1990

A:Title: Rubisco genes indicate a close phylogenetic relation between the plastids of Ch

A:Reference number: S13123; MUID:91338696

A:Accession: S13124

A:Molecule type: DNA

A:Residues: 1-139 <VAL>

A:Cross-references: EMBL:X52503; NID:g11543; PIDN:CAA36744.1; PID:g11545

C:Genetics:

A:Gene: chloroplast

C:Superfamily: ribulose-bisphosphate carboxylase small chain

C:Keywords: Calvin cycle; carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase; c

Query Match 35.5%; Score 44; DB 1; Length 139;

Best Local Similarity 45.5%; Pred. No. 25;

Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

QY 6 SFEWT--PY----YQWPVALPL 21

||||:||||:||||:

Db 34 SVEWTDPPRNSYWELWGLPL 55

RESULT 10

RKPSL

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain - brown alga (Pylaiella l

C:Species: Chloroplast Pylaiella littoralis

C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999

C:Accession: S17764

R:Assali, N.E.; Martin, W.F.; Somerville, C.C.; Loiseau-de Goer, S.

Plant Mol. Biol. 17, 853-863, 1991

A:Title: Evolution of the Rubisco operon from prokaryotes to algae: structure and ana

A:Reference number: S17764; MUID:92003695

A:Accession: S17764

A:Molecule type: DNA

A:Residues: 1-139 <ASS>

A:Cross-references: EMBL:X55372; NID:g14186; PIDN:CAA39052.1; PID:g14188

C:Genetics:

A:Gene: rbcS

A:Genome: chloroplast

C:Superfamily: ribulose-bisphosphate carboxylase small chain

C:Keywords: Calvin cycle; carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase

Query Match 35.5%; Score 44; DB 1; Length 139;

Best Local Similarity 45.5%; Pred. No. 25;

Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

QY 6 SFEWT--PY----YQWPVALPL 21

||||:||||:||||:

Db 34 SVEWTDPPRNSYWELWGLPL 55

RESULT 11

E70530

hypothetical protein Rv2698 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: E70530

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; MUID:98295987

A:Accession: E70530

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-161 <COL>

A:Cross-references: GB:X96072; GB:AL123456; NID:g3261793; PIDN:CAB09488.1; PID:g21819

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: Rv2698

C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2698

Query Match 35.5%; Score 44; DB 2; Length 161;

Best Local Similarity 46.2%; Pred. No. 29;

Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 9 WTPYYQWPVALPL 21

||||:||||:||||:

Db 18 WVPWWWWPLAFAL 30

RESULT 14

S48466
MOBI protein [validated] - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YIL106w
C:Species: Saccharomyces cerevisiae
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C:Accession: S48466
R:Bowman, S.; Churcher, C.
submitted to the EMBL Data Library, September 1994
A:Reference number: S48455
A:Accession: S48466
A:Molecule type: DNA
A:Residues: 1-314 <BOW>
A:Cross-references: EMBL:Z38125; NID:g558688; PIDN:CAA86274.1; PID:g558700; GSPDB:GNO
R:Luca, F.C.; Winey, M.
Mol. Biol. Cell 9, 29-46, 1998
A:Title: MOBI, an essential yeast gene required for completion of mitosis and mainten
A:Reference number: A59298; MUID:98099687
A:Contents: annotation
C:Genetics:
A:Gene: SGD:MOB1; MIPS:YIL106w
A:Cross-references: SGD:S0001368; MIPS:YIL106w
A:Map position: 9L
A:Introns: 7/2
C:Function:
A:Description: required for normal cell cycle progression; required for completion of
C:Superfamily: Saccharomyces cerevisiae mob1 protein
C:Keywords: phosphoprotein

| | | | | |
|-----------------------|-------|---------------|-------|-------------|
| Query Match | 35.5% | Score 44; | DB 1; | Length 314; |
| Best Local Similarity | 38.9% | Pred. NO. 58; | | |
| Matches | 7; | Conservative | 5; | Mismatches |
| | | | 6; | Indels |
| | | | 0; | Gaps |

RESULT 15
T25055
hypothetical protein T21B4.9 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T25055
R:Smye, R.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19974
A:Accession: T25055
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-334 <WIL>
A:Cross-references: EMBL:Z81124; PIDN:CAB03376.1; GSPDB:GN00020; CESP:T21B4.9
A:Experimental source: clone T21B4
C:Genetics:
A:Gene: CESP:T21B4.9
A:Map position: 2
A:Introns: 120/1; 183/3
C:Superfamily: *Caenorhabditis* hypothetical protein C49G7.2

| | Matches | 7; Conservative | 3; Mismatches | 2; Indels | 0; Gaps | 0; |
|----|---------|-----------------|---------------|-----------|---------|----|
| Qy | 6 | SFEWTPYYWQPY | 17 | | | |
| | | : : : | | | | |
| Db | 80 | SFEFTPEYILPY | 91 | | | |

Search completed: August 16, 2001, 14:54:29
Job time: 40 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 17, 2001, 07:37:22 ; Search time 10.07 Seconds
(without alignments)
72.656 Million cell updates/sec

Title: US-09-428-082-213
Perfect score: 124
Sequence: 1 TANVSSEFWTPYWPYALPL 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

atched: 94743 seqs, 34840360 residues

Total number of hits satisfying chosen parameters: 94743

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|----------------------|
| 1 | 50 | 40.3 | 549 | 1 BETA_RHIME | P54223 rhizobium m |
| 2 | 46 | 37.1 | 1193 | 1 ACE_CHICK | Q10751 gallus gall |
| 3 | 44.5 | 35.9 | 664 | 1 Y4FE_RHISN | P55440 rhizobium s |
| 4 | 44 | 35.5 | 139 | 1 RBS_ECTSI | P24395 ectocarpus |
| 5 | 44 | 35.5 | 139 | 1 RBS_PYLII | P23652 pylaieiella 1 |
| 6 | 44 | 35.5 | 236 | 1 MOB1_YEAST | P40484 saccharomyc |
| 7 | 44 | 35.5 | 420 | 1 DHE3_PYRAB | Q47950 pyrococcus |
| 8 | 44 | 35.5 | 420 | 1 DHE3_PYREN | Q47951 pyrococcus |
| 9 | 44 | 35.5 | 420 | 1 DHE3_PYRFU | P80319 pyrococcus |
| 10 | 44 | 35.5 | 420 | 1 DHE3_PYRHO | O52310 pyrococcus |
| 11 | 44 | 35.5 | 427 | 1 MFGM_BOVIN | O95114 bos taurus |
| 12 | 44 | 35.5 | 772 | 1 YICI_ECOLI | P31434 escherichia |
| 13 | 43.5 | 35.1 | 283 | 1 YMX8_CAEEL | P34516 caenorhabdi |
| 14 | 43 | 34.7 | 198 | 1 LEUD_MYCTU | O53236 mycobacteri |
| 15 | 43 | 34.7 | 297 | 1 SC13_YEAST | Q04491 saccharomyc |
| 16 | 43 | 34.7 | 342 | 1 VATC_ARCFU | O29103 archaeoglob |
| 17 | 43 | 34.7 | 434 | 1 BZTC_RHOCA | O52665 rhodobacter |
| 18 | 43 | 34.7 | 437 | 1 HGD_CAEEL | O9Y041 caenorhabdi |
| 19 | 43 | 34.7 | 478 | 1 CYCA_GLUSU | Q47945 gluconobact |
| 20 | 43 | 34.7 | 529 | 1 YBB1_BACSU | P40408 bacillus su |
| 21 | 42.5 | 34.3 | 159 | 1 Y131_AGRTO | P05680 agrobacteri |
| 22 | 42.5 | 34.3 | 275 | 1 FLA5_PYRKO | O9V247 pyrococcus |
| 23 | 42.5 | 34.3 | 367 | 1 YMW7_YEAST | Q03151 saccharomyc |
| 24 | 42 | 33.9 | 150 | 1 YD06_YEAST | P38955 saccharomyc |
| 25 | 42 | 33.9 | 191 | 1 Y611_METJA | Q58028 methanococc |
| 26 | 42 | 33.9 | 535 | 1 XYNB_BACPU | P07129 bacillus pu |
| 27 | 42 | 33.9 | 562 | 1 GUN1_ACICE | P54583 acidothermu |
| 28 | 42 | 33.9 | 562 | 1 YFAA_ECOLI | P17994 escherichia |
| 29 | 42 | 33.9 | 956 | 1 RRPO_SBMV | P21405 southern be |
| 30 | 42 | 33.9 | 1086 | 1 CHSD_EMENI | P78611 emericella |
| 31 | 42 | 33.9 | 1184 | 1 CHSE_EMENI | Q00744 emericella |
| 32 | 41.5 | 33.5 | 230 | 1 COX2_BRAFL | O47428 branchiosto |
| 33 | 41.5 | 33.5 | 239 | 1 COX2_BRALA | O79417 branchiosto |

RESULT 1

| ID | BETA_RHIME | STANDARD | PRT | 549 AA |
|----|--|----------|-----|--------|
| AC | P54223 | | | |
| DT | 01-OCT-1996 (Rel. 34, Created) | | | |
| DT | 30-MAY-2000 (Rel. 39, Last sequence update) | | | |
| DT | 30-MAY-2000 (Rel. 39, Last annotation update) | | | |
| DE | CHOLINE DEHYDROGENASE (EC 1.1.99.1) (CHD). | | | |
| GN | BETA. | | | |
| OS | Rhizobium meliloti (Sinorhizobium meliloti). | | | |
| OC | Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; | | | |
| OC | Rhizobiaceae; Sinorhizobium. | | | |
| OX | NCBI_Taxid=382; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=102F34; | | | |
| RX | MEDLINE=97286552; PubMed=9141699; | | | |
| RA | Poccard J.A., Vincent N., Boncompagni E., Tombras Smith L., | | | |
| RA | Poggi M.-C., Le Rudulier D.; | | | |
| RT | "Molecular characterization of the bet genes encoding glycine betaine | | | |
| RT | synthesis in Sinorhizobium meliloti 102F34."; | | | |
| RL | Microbiology 143:1369-1379(1997). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=1021; | | | |
| RA | Galibert F., Capela D., Hubler-Barloy F., Gatiou M., Batut J., | | | |
| RA | Bolstead P., Gouzy J., Kahn D., Thebault P., Goffeau A., | | | |
| RA | Purnelle B., Pohl T., Bothe G., Schneider S., Portetel D., | | | |
| RA | Vandenbol M., Puehler A., Becker A., Weidner S.; | | | |
| RL | Submitted (MAR-2000) to the SWISS-PROT data bank. | | | |
| CC | -!- FUNCTION: CAN CATALYZE THE OXIDATION OF CHOLINE TO BETAINE | | | |
| CC | ALDEHYDE & BETAINE ALDEHYDE TO GLYCINE BETAINE AT THE SAME RATE. | | | |
| CC | IT IS INDEPENDENT OF SOLUBLE COFACTORS, AND PROBABLY ELECTRON- | | | |
| CC | TRANSFER-LINKED (BY SIMILARITY). | | | |
| CC | -!- CATALYTIC ACTIVITY: CHOLINE + ACCEPTOR = BETAINE ALDEHYDE + | | | |
| CC | REDUCED ACCEPTOR. | | | |
| CC | -!- COFACTOR: FAD. | | | |
| CC | -!- PATHWAY: OSMOREGULATORY CHOLINE-GLYCINE BETAINE PATHWAY. | | | |
| CC | -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. | | | |
| CC | -!- SIMILARITY: BELONGS TO THE GMC OXIDOREDUCTASES FAMILY. | | | |
| CC | ----- | | | |
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| CC | or send an email to license@isb-sib.ch). | | | |
| CC | ----- | | | |
| CC | EMBL; U39940; AAC13369.1; .. | | | |
| CC | InterPro; IPR000172; GMC_Oxred. | | | |
| DR | InterPro; IPR000205; NAD_Binding. | | | |
| DR | Pfam; PF007732; GMC_Oxred; 1. | | | |
| DR | PROSITE; PS00623; GMC_OXRED_1; 1. | | | |
| DR | PROSITE; PS00624; GMC_OXRED_2; 1. | | | |
| KW | Oxidoreductase; Flavoprotein; FAD; Membrane. | | | |

P28817 saccharomyc
P41647 pinus thunb
P75337 mycoplasma
P20956 xenopus lae
P24683 cylindrothe
P49521 odontella s
P14961 olisthodisc
Q94165 caenorhabdi
P12424 nicotiana p
Q9vuk5 drosophila
O75844 homo sapien
P38741 saccharomyc

ALIGNMENTS

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FT NP_BIND 4 33 FAD (ADP PART) (PROBABLE).
FT ACT_SITE 470 470 POTENTIAL.
FT CONFLICT 267 267 A -> R (IN REF. 1).
FT CONFLICT 417 424 RHCVRLTR -> DLRAVTV (IN REF. 1).
FT CONFLICT 429 429 Q -> E (IN REF. 1).
SQ SEQUENCE 549 AA; 61291 MW; 29BE064F40CB88F4 CRC64;

Query Match 40.3%; Score 50; DB 1; Length 549;
Best Local Similarity 44.4%; Pred. No. 9.4;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 TANVSSFETPTYPYWPYA 18
| | | | | | | | | |
DB 301 TRPVSLYSLPWFQGV 318

RESULT 2
ID ACE_CHECK STANDARD; PRT; 1193 AA.
AC Q10751;
Q1-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
DE ANGIOTENSIN-CONVERTING ENZYME (EC 3.4.15.1) (DIPEPTIDYL
GN CARBOXYPEPTIDASE I) (KININASE II) (FRAGMENT).
OS Gallus.
OC Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Lung;
RX MEDLINE=95110342; PubMed=7811282;
RA Esther C.R., Thomas K.E., Bernstein K.E.;
RT "Chicken lacks the testis specific isozyme of angiotensin converting
enzyme found in mammals.";
RL Biochem. Biophys. Res. Commun. 205:1916-1921(1994).
CC -!- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF
THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE
VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.
CC -!- CATALYTIC ACTIVITY: RELEASE OF A C-TERMINAL DIPEPTIDE,
OLIGOPEPTIDE-|-XAA-XBB, WHEN XAA IS NOT PRO, AND XBB IS NEITHER
ASP NOR GLU. CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II.
CC -!- COPACITOR: BINDS TWO ZINC IONS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2 (ZINC METALLOPROTEASE).
-----
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-----
EMBL; L40175; AAA75554.1; -
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR000130; Zn_Mtpeptdse.
DR Pfam; PF01401; Peptidase_M2; 2.
DR ProDom; PD004184; -; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; 2.
KW Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
KW Glycoprotein; Transmembrane; Duplication.
FT NON_TER 1 1
FT DOMAIN <1 1156 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1157 1173 POTENTIAL.
FT DOMAIN 1174 1193 CYTOPLASMIC (POTENTIAL).
FT REPEAT 125 481
FT REPEAT 723 1079
FT METAL 288 288 ZINC 1 (CATALYTIC) (BY SIMILARITY).

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FT ACT_SITE 289 289 1 (BY SIMILARITY).
FT METAL 292 292 ZINC 1 (CATALYTIC) (BY SIMILARITY).
FT METAL 886 886 ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 887 887 2 (BY SIMILARITY).
FT METAL 890 890 ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 11 11 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 60 60 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 485 485 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 513 513 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 555 555 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 575 575 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 658 658 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1089 1089 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1193 AA; 137820 MW; 954472A18EA471C7 CRC64;

Query Match 37.1%; Score 46; DB 1; Length 1193;
Best Local Similarity 42.1%; Pred. No. 66;
Matches 8; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 1 TANVSSFETPTYPYWPYA 19
| | | | | | | | | |
DB 1111 TENGEVLGMPEYSWTPYAV 1129

RESULT 3
Y4FB_RHISN STANDARD; PRT; 664 AA.
ID Y4FB_RHISN STANDARD; PRT; 664 AA.
AC P55440;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 73.7 KDA PROTEIN Y4FB.
GN Y4FB.
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
CC -!- SIMILARITY: NONE OBVIOUS.
-----
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-----
EMBL; AE000072; AAB91659.1; -
DR InterPro; IPR001604; Endonuclease.
DR SMART; SM00477; NUC; 1.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 664 AA; 73731 MW; CFCC041FB73C064F CRC64;

Query Match 35.9%; Score 44.5; DB 1; Length 664;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 8; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 2 ANVSSFETPTYPYWPYA 14
| | | | | | | |
DB 506 ANDDTFQWNTNCSQYW 521

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RESULT 4
RBS_ECTSI          STANDARD; .      PRT; 139 AA.
AC P24395;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RUBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN (EC 4.1.1.39) (RUBISCO
DE SMALL SUBUNIT).
GN RBES.
OS Ectocarpus siliculosus.
OG Chloroplast.
OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales; Ectocarpaceae;
OC Ectocarpus.
OX NCBI_TaxID=2880;
[1]
SEQUENCE FROM N.A.
STRAIN=DILLWIN (LYNGBYE);
RX MEDLINE=91338696; PubMed=2102375;
RA Valentin K., Zetsche K.;
RT "Rubisco genes indicate a close phylogenetic relation between the
RT plastids of Chromophyta and Rhodophyta.";
RL Plant Mol. Biol. 15:575-584(1990).
CC -1- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF
CC D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
CC THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
CC ACTIVE SITE.
CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) =
CC 2 3-PHOSPHO-D-GLYCERATE.
CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) =
CC 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
CC -1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
CC
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CC -----
CC EMBL; X52503; CAA36744.1; -.
CC PIR; S13124; RKAUS.
CC DR HSSP; P04716; LRSC.
CC DR Mendel; 4963; ECTS1; rbs; 1.
CC DR InterPro; IPR000894; RuBisCO_small.
CC DR Pfam; PF00101; RuBisCO_small; 1.
CC DR ProDom; PD000290; -. 1.
CC DR Photosynthesis; Carbon dioxide fixation; Photorespiration; Lyase;
CC KW Oxidoreductase; Monooxygenase; Chloroplast.
CC SQ SEQUENCE 139 AA; 15938 MW; E316D7803358702D CRC64;

Query Match 35.5%; Score 44; DB 1; Length 139;
Best Local Similarity 45.5%; Pred. No. 17;
Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

QY 6 SFEWT--PY-----YQOPYALPL 21
| | | | | : | | | | |
Db 34 SVEWTDPPHPRNSYWLWGLPL 55

RESULT 5
RBS_PYLII
ID *RBS_PYLII          STANDARD;          PRT; 139 AA.
AC P23652;
DT 01-NOV-1991 (Rel. 20, Created)

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DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RUBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN (EC 4.1.1.39) (RUBISCO
DE SMALL SUBUNIT).
GN RBES.
OS Pyraliella littoralis.
OG Chloroplast.
OC Eukaryota; stramenopiles; Phaeophyceae; Ectocarpales;
OC Acinetosporaceae; Pyraliella.
OX NCBI_TaxID=2885;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=91355877; PubMed=2103450;
RA Assali N.E., Mache R., Loiseaux-De Goer S.;
RT "Evidence for a composite phylogenetic origin of the plastid genome
RT of the brown alga Pyraliella littoralis (L.) Kjellm.";
RL Plant Mol. Biol. 15:307-315(1990).
[2]
SEQUENCE FROM N.A.
RX MEDLINE=92003695; PubMed=1840691;
RA Assali N.E., Martin W.F., Sommerville C.C., Loiseaux-De Goer S.;
RT "Evolution of the Rubisco operon from prokaryotes to algae: structure
RT and analysis of the rbcS gene of the brown alga Pyraliella
RT littoralis.";
RL Plant Mol. Biol. 17:853-863(1991).
CC -1- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF
CC D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
CC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
CC THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
CC REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
CC ACTIVE SITE.
CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) =
CC 2 3-PHOSPHO-D-GLYCERATE.
CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) =
CC 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
CC -1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- MISCELLANEOUS: IN THIS ALGA, IN CONTRAST TO PLANTS, THE SMALL
CC SUBUNIT IS ENCODED IN THE CHLOROPLAST.
CC -1- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
CC
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CC -----
CC EMBL; X55372; CAA39052.1; -.
CC PIR; S17764; RKPFSL.
CC DR HSSP; P04716; LRSC.
CC DR Mendel; 4021; PYLII; rbs; 1.
CC DR InterPro; IPR000894; RuBisCO_small.
CC DR Pfam; PF00101; RuBisCO_small; 1.
CC DR ProDom; PD000290; -. 1.
CC DR Photosynthesis; Carbon dioxide fixation; Photorespiration; Lyase;
CC KW Oxidoreductase; Monooxygenase; Chloroplast.
CC SQ SEQUENCE 139 AA; 15897 MW; 075DC3800915DDC5 CRC64;

Query Match 35.5%; Score 44; DB 1; Length 139;
Best Local Similarity 45.5%; Pred. No. 17;
Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

QY 6 SFEWT--PY-----YQOPYALPL 21
| | | | | : | | | | |
Db 34 SVEWTDPPHPRNSYWLWGLPL 55

RESULT 6
MOBI_YEAST
ID MOBI_YEAST          STANDARD;          PRT; 236 AA.

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AC P40484;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MOBI PROTEIN (MPS1 BINDER 1).
GN MOBI OR YIL106W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
RA Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
RA Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
RA Walsh S.V., Whitehead S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: REQUIRED FOR NORMAL CELL PROGRESSION.
CC -!- SIMILARITY: TO YEAST MOBI.
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CC -----
CC EMBL; Z38125; CAA86274.1; ALT_INIT.
CC SGD; S0001368; MOBI.
CC SEQUENCE 236 AA; 27413 MW; B9EA7B36F385D08 CRC64;
DR
SQ
Query Match 35.5%; Score 44; DB 1; Length 236;
Best Local Similarity 38.9%; Pred. NO. 28;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 3 NVSSFEWTPYMQPYALP 20
DB 20 NVTDFNTPSHQKPLQP 37
||:||||:|:|:|
RESULT 7
DHE3_PYRAB STANDARD; PRT; 420 AA.
ID DHE3_PYRAB
AC Q47950;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMATE DEHYDROGENASE (EC 1.4.1.3) (GDH).
GN GDH OR GDH OR PAB0391.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORSAY;
RA Hellig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE OF 22-255 FROM N.A.
RC STRAIN=GES;
RA Borges K.M., Diruggiero J., Robb F.T.;
RT "Cloning and sequencing of glutamate dehydrogenases from
RT hyperthermophilic archaea.";
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: L-GLUTAMATE + H(2)O + NAD(P)(+) =
CC 2-OXOGLUTARATE + NH(3) + NAD(P)H.
CC -----
CC EMBL; L12408; AAA64795.1;
CC InterPro; IPR001625; GLFV_dehydrog.
CC Pfam; PF00208; GLFV_dehydrog; 1.
CC PRINTS; PS00082; GLFVDRGNASE.
CC PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
CC -!- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
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CC -----
CC EMBL; AJ248284; CAB49491.1;
CC EMBL; LI9116; AAA64796.1;
CC HSP; P80319; IGTW.
CC InterPro; IPR001625; GLFV_dehydrog.
CC Pfam; PF00208; GLFV_dehydrog; 2.
CC PRINTS; PS00082; GLFVDRGNASE.
CC PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
KW Oxidoreductase; NAD; NADP.
FT ACT_SITE 105 105 BY SIMILARITY.
FT NP_BIND 220 226 NAD (POTENTIAL).
FT SEQUENCE 420 AA; 47098 MW; 82F8B343572DFE2B CRC64;
DR
SQ
Query Match 35.5%; Score 44; DB 1; Length 420;
Best Local Similarity 60.0%; Pred. NO. 47;
Matches 9; Conservative 0; Mismatches 2; Indels 4; Gaps 1;
QY 4 VSSFEW---TPYYW 14
DB 351 VSFEWQNTGYW 365
||| ||| |||
RESULT 8
DHE3_PYREN STANDARD; PRT; 420 AA.
ID DHE3_PYREN
AC Q47951;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GLUTAMATE DEHYDROGENASE (EC 1.4.1.3) (GDH).
GN GDH.
OS Pyrococcus endeavori.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=39456;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=ES4;
RX MEDLINE=93352584; PubMed=8349661;
RA Diruggiero J., Robb F.T., Jagus R., Klump H.H., Borges K.M.,
RA Kessel M., Mai X., Adams M.W.A.;
RT "Characterization, cloning, and in vitro expression of the extremely
RT thermostable glutamate dehydrogenase from the hyperthermophilic
RT Archaeon, ES4.";
RL Biol. Chem. 268:17767-17774(1993).
CC -!- CATALYTIC ACTIVITY: L-GLUTAMATE + H(2)O + NAD(P)(+) =
CC 2-OXOGLUTARATE + NH(3) + NAD(P)H.
CC -!- SUBUNIT: HOMOHEXAMER.
CC -!- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
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CC -----
CC EMBL; L12408; AAA64795.1;
CC InterPro; IPR001625; GLFV_dehydrog.
CC Pfam; PF00208; GLFV_dehydrog; 1.
CC PRINTS; PS00082; GLFVDRGNASE.
CC PROSITE; PS00074; GLFV_DEHYDROGENASE; 1.
```



```
KW Oxidoreductase; NAD; NADP.
FT ACT_SITE 105 105 BY SIMILARITY.
FT NP_BIND 220 226 NAD (POTENTIAL).
SQ SEQUENCE 420 AA; 47141 MW; 26C571CC5DEF85CB CRC64;

Query Match 35.5%; Score 44; DB 1; Length 420;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

QY 4 VSSFEEW----TPYYW 14
DB 351 VSYFEWQNTGYW 365

RESULT 9
DHE3_PYRFU STANDARD; PRT; 420 AA.
P80319;
01-JUN-1994 (Rel. 29, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DE GLUTAMATE DEHYDROGENASE (EC 1.4.1.3) (GDH).
GN GDHA OR GDH.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_Taxid=2261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94010338; PubMed=8406037;
RA Eggen R.I.L., Geerling A.C.M., Waldkoetter K., Antranikian G.,
de Vos V.M.;
RT "The glutamate dehydrogenase-encoding gene of the hyperthermophilic
archaeon Pyrococcus furiosus: sequence, transcription and analysis of
the deduced amino acid sequence.";
RL Gene 132:143-148(1993).
RN [2]
RP SEQUENCE.
RC STRAIN=DSM 3638;
RX MEDLINE=94338538; PubMed=8060497;
RA Maras B., Vallante S., Chiaraluce R., Consalvi V., Politi L.,
de Rosa M., Bossa F., Scandurra R., Barra D.;
RT "The amino acid sequence of glutamate dehydrogenase from Pyrococcus
furiosus, a hyperthermophilic archaeobacterium.";
RL J. Protein Chem. 13:253-259(1994).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=96164432; PubMed=8591026;
RA Yip K.S.P., Stillman T.J., Britton K.L., Artymiuk P.J., Baker P.J.,
Sedelnikova S.E., Engel P.C., Pasquo A., Chiaraluce R., Consalvi V.,
Scandurra R., Rice D.W.;
RT "The structure of Pyrococcus furiosus glutamate dehydrogenase reveals
a key role for ion-pair networks in maintaining enzyme stability at
extreme temperatures.";
RL Structure 3:1147-1158(1995).
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE + H(2)O + NAD(P)(+) =
2-OXOGLOUTARATE + NH(3) + NAD(P)H.
CC -1- SUBUNIT: HOMOHETEROMER.
CC -1- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
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CC -----
CC EMBL: M97860; AAA8390.1;
DR PIR: JN0854; JN0854
DR FDB: IGM7; 11-JAN-97.
DR InterPro: IPR001625; GLFV_dehydrog.
DR Pfam: PF00208; GLFV_dehydrog; 1.

PRINTS: PR00082; GLFDHGRGNASE.
PROSITE: PS00074; GLFV_DEHYDROGENASE; 1.
Oxidoreductase; NAD; NADP; 3D-structure.
FT ACT_SITE 105 105 NAD (POTENTIAL).
FT NP_BIND 220 226 NAD (POTENTIAL).
FT CONFLICT 366 366 AW -> WA (IN REF. 2).
FT CONFLICT 366 366 T -> K (IN REF. 2).
SQ SEQUENCE 420 AA; 47114 MW; 673DB20F8764A93C CRC64;

Query Match 35.5%; Score 44; DB 1; Length 420;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

QY 4 VSSFEEW----TPYYW 14
DB 351 VSYFEWQNTGYW 365

RESULT 10
DHE3_PYRHO STANDARD; PRT; 420 AA.
AC 052310;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLUTAMATE DEHYDROGENASE (EC 1.4.1.3) (GDH).
GN GDHA OR GDH OR PH1593.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_Taxid=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL;
RA Gonzalez J.M., Robb F.T., Kato C.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE + H(2)O + NAD(P)(+) =
2-OXOGLOUTARATE + NH(3) + NAD(P)H.
CC -1- SUBUNIT: HOMOHETEROMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
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CC -----
CC EMBL: AF035935; AAB99956.1;
DR EMBL: AP000006; BAA30705.1; ALT_INIT.
DR InterPro: IPR001625; GLFV_dehydrog.
DR Pfam: PF00208; GLFV_dehydrog; 1.
PRINTS: PR00082; GLFDHGRGNASE.
PROSITE: PS00074; GLFV_DEHYDROGENASE; 1.
Oxidoreductase; NAD; NADP.
FT ACT_SITE 105 105 BY SIMILARITY.
FT NP_BIND 220 226 NAD (POTENTIAL).
SQ SEQUENCE 420 AA; 47014 MW; 1198BEC2681B5AA2 CRC64;
```

Query Match 35.5%; Score 44; DB 1; Length 420;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 9; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

QY 4 VSSFEEW---TPYYW 14

DB 351 VSYFEWQNTGYW 365

RESULT 11

MEGM_BOVIN STANDARD; PRT; 427 AA.
AC Q95114; Q27959; P79344;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LACTADHERIN PRECURSOR (MILK FAT GLOBULE-EGF FACTOR 8) (MFG-E8)
DE (MGP57/53) (PAS-6/PAS-7 GLYCOPROTEIN) (MEGM) (SPERM SURFACE PROTEIN
DE SP47) (BP47) (COMPONENTS 15/16).
GN MFG-E8.

Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.

NCBI_TaxID=9913;

[1]

SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CARBOHYDRATE-LINKAGE SITES.

RP STRAIN-HOLSTEIN; TISSUE=Mammary gland;

RX MEDLINE-97008954; PubMed-8956064;

RA Hvarrregaard J., Andersen M.H., Berglund L., Rasmussen J.T.,

RA Petersen T.E.;

RT "Characterization of glycoprotein PAS-6/7 from membranes of bovine

RT milk fat globules.";

RL Eur. J. Biochem. 240:628-636(1996).

[2]

SEQUENCE OF 18-427 FROM N.A.

RP TISSUE=Mammary gland;

RX MEDLINE-96125736; PubMed-8541316;

RA Aoki N., Kishi M., Taniguchi Y., Adachi T., Nakamura R.,

RA Matsuda T.;

RT "Molecular cloning of glycoprotein antigens MGP57/53 recognized by

RT monoclonal antibodies raised against bovine milk fat globule

RT membrane.";

RL Biochim. Biophys. Acta 1245:385-391(1995).

[3]

SEQUENCE OF 19-427 FROM N.A.

RP TISSUE-Testis;

RA Ensslin M.A.;

RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

[4]

SEQUENCE OF 140-146; 174-187; 233-246 AND 422-427.

RP TISSUE=Milk;

RX MEDLINE-93250576; PubMed-8485470;

RA Mather I.H., Banghart L.R., Lane W.S.;

RT "The major fat-globule membrane proteins, bovine components 15/16 and

RT guinea-pig GP 55, are homologous to MGF-E8, a murine glycoprotein

RT containing epidermal growth factor-like and factor V/VIII-like

RT sequences.";

RL Biochem. Mol. Biol. Int. 29:545-554(1993).

-1- FUNCTION: PROBABLY ASSOCIATES WITH PHOSPHOLIPIDS ON THE SURFACE OF

CC MAMMARY EPITHELIAL CELLS AND MILK FAT GLOBULES. ZONA PELLUCIDA-

CC BINDING PROTEIN.

-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A

CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING. THE SHORT FORM

CC LACKS 53 AMINO ACIDS WITHIN THE F5/8 TYPE C 1 DOMAIN.

-1- TISSUE SPECIFICITY: MILK AND SPERMATOZOAN.

-1- PTM: THE 2 O-LINKED GLYCANS CONSIST OF GAL, GLCNAC AND FUC, WITH

CC PROBABLY FUC AS REDUCING TERMINAL SUGAR.

-1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

-1- SIMILARITY: CONTAINS 2 F5/8 TYPE C DOMAINS.

CC -----

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CC -----

CC EMBL; X91895; CAA62997.1; -

DR EMBL; S80643; AAB35894.2; -

DR EMBL; Y11719; CAA72406.1; -

DR HSP; P00740; LIXA

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR000421; FAS8_C.

DR Pfam: PF00008; EGF; 2.

DR Pfam: PF00754; F5_F8_type_C; 2.

DR SMART; SM00181; EGF; 2.

DR SMART; SM00231; FAS8C; 2.

DR PROSITE; PS00022; EGF_1; 2.

DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01285; FAS8C_1; 2.

DR PROSITE; PS01286; FAS8C_2; 2.

KW Signal; Glycoprotein; Milk; Repeat; EGF-like domain;

KW Alternative splicing

FT SIGNAL 1 18

FT CHAIN 19 427 LACTADHERIN.

FT DOMAIN 20 59 EGF-LIKE 1.

FT DOMAIN 62 106 EGF-LIKE 2.

FT DOMAIN 109 265 F5/8 TYPE C 1.

FT DOMAIN 270 427 F5/8 TYPE C 2.

FT SITE 85 87 CELL ATTACHMENT SITE (POTENTIAL).

FT DISULFID 24 35 BY SIMILARITY.

FT DISULFID 29 47 BY SIMILARITY.

FT DISULFID 49 58 BY SIMILARITY.

FT DISULFID 66 77 BY SIMILARITY.

FT DISULFID 71 94 BY SIMILARITY.

FT DISULFID 96 105 BY SIMILARITY.

FT DISULFID 109 265 BY SIMILARITY.

FT DISULFID 252 256 BY SIMILARITY.

FT DISULFID 270 427 BY SIMILARITY.

FT CARBOHYD 27 27 O-LINKED (FUC. . .) (IN PAS-6).

FT CARBOHYD 34 34 O-LINKED (FUC. . .) (IN PAS-7).

FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (HYBRID) (IN PAS-6

AND PAS-7).

FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .) (HIGH MANNOSE) (IN

PAS-6).

FT VARSPIC 169 221 MISSING (IN SHORT ISOFORM).

FT CONFLICT 19 19 A -> F (IN REF. 1).

FT CONFLICT 28 28 L -> Q (IN REF. 1).

SQ SEQUENCE 427 AA; 47411 MW; 4CBEE3A1DC4EB24 CRC64;

Query Match 35.5%; Score 44; DB 1; Length 427;

Best Local Similarity 53.8%; Pred. No. 48;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 TANVSSFEPY 13

DB 294 TWGLSAFSPY 306

RESULT 12

YICL_ECOLI

ID YICL_ECOLI STANDARD; PRT; 772 AA.

AC P31434; P76723;

DT 01-JUL-1993 (Rel. 26, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE HYPOTHETICAL 88.1 KDA PROTEIN IN GLTS-SELC INTERGENIC REGION.

GN YICL OR B3656.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562;

```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=K12 / MGI655;
RX  MEDLINE=93315143; PubMed=766882;
RA  Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
RT  "DNA sequence and analysis of 136 kilobases of the Escherichia coli
RL  genome: organizational symmetry around the origin of replication.";
CC  Genomics 16:551-561(1993).
CC  -1- SIMILARITY: TO E.HERBICOLA HYPOTHETICAL PROTEIN IN CRTE 3'REGION
CC  (ORF2) (AC Q01336).
CC  -----
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CC  -----
EMBL; LI0328; AAG2009.1; -
DR  EMBL; AE000443; AAC76680.1; -
DR  EcoGene; EGI1685; Yici.
DR  InterPro: IPR000322; Glyco_hydro_31.
DR  Pfam: PF01055; Glyco_hydro_31; 1.
KW  Hypothetical protein.
SQ  SEQUENCE 772 AA; 88079 MW; 6F2A02E4B5403772 CRC64;

Query Match 35.5%; Score 44; DB 1; Length 772;
Best Local Similarity 29.4%; Pred. No. 82;
Matches 5; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 4 VSSFEWTPPYWQYPALP 20
DB 310 MKAFQWCFDFWDLPTFP 326
:|:|:|:|:|

RESULT 13
YMX8-CAEEL STANDARD; PRT; 283 AA.
AC P34516;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE HYPOTHETICAL 32.6 KDA PROTEIN K06H7.8 IN CHROMOSOME III.
K06H7.8.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kerhaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
RA Silms M., Smalton M., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
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CC -----
DR EMBL; LI5314; AAA28091.1; -
DR PIR; S44848; S44848.
DR HSP; Q06486; ICKI.
DR WormPep; K06H7.8; CE00259.
KW Hypothetical protein.
SQ SEQUENCE 283 AA; 32597 MW; 84492C4D99984296 CRC64;

Query Match 35.1%; Score 43.5; DB 1; Length 283;
Best Local Similarity 38.5%; Pred. No. 38;
Matches 5; Conservative 7; Mismatches 0; Indels 1; Gaps 1;

QY 5 SSFEWT-PYYWQP 16
DB 227 ANYRWSDDPIHWP 239
:::|:|:|:|:|

RESULT 14
LEUD_MYCTU STANDARD; PRT; 198 AA.
ID LEUD_MYCTU
AC O53236;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 3-ISOPROPYLMALATE DEHYDRATASE SMALL SUBUNIT (EC 4.2.1.33)
DE (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI).
GN LEUD OR RV2987C OR MTV012.01C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,
RA Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
CC -1- CATALYTIC ACTIVITY: 3-ISOPROPYLMALATE = 2-ISOPROPYLMALATE +
CC H(2)O (ALSO CATALYSES 2-ISOPROPYLMALATE + H(2)O = 3-HYDROXY-
CC 4-METHYL-3-CARBOXPENTANONE).
CC -1- PATHWAY: SECOND STEP IN LEUCINE BIOSYNTHESIS.
CC -1- SUBUNIT: CONSISTS OF TWO DIFFERENT SUBUNITS: LEUC AND LEUD.
CC -----
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CC -----
DR EMBL; AL021287; CAA16072.1; -
DR TuberculList; RV2987c; -
DR InterPro: IPR000573; Aconitase_C.
DR Pfam: PF00694; Aconitase_C.1.
KW Leucine biosynthesis; Lyase.
SQ SEQUENCE 198 AA; 21780 MW; 705B4A11FB41DB8B CRC64;

Query Match 34.7%; Score 43; DB 1; Length 198;
```

```

DR EMBL; U14913; AAB67426.1; -.
DR PIR; S30803; S30803.
DR PIR; A45442; A45442.
DR PIR; S48559; S48559.
DR SGD; S0004198; SEC13.
DR InterPro; IPR001680; WD40.
DR Pfam; PF004000; WD40; 6.
DR PRINTS; PR00320; GPROTEINBRPT.
DR SMART; SM00320; WD40; 6.
DR PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
DR PROSITE; PS50082; WD_REPEATS_2; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
DR KW Transport; Protein transport; Membrane; Endoplasmic reticulum;
DR KW Repeat; WD repeat.
DR REPEAT 37 WD 1.
DR REPEAT 51 WD 2.
DR REPEAT 97 WD 3.
DR REPEAT 143 WD 4.
DR REPEAT 202 WD 5.
DR REPEAT 252 WD 6.
DR REPEAT 224 S->K: GROWTH INHIBITED ABOVE 30 C.
DR MUTAGEN 224 W->R: GROWTH INHIBITED ABOVE 30 C.
DR MUTAGEN 262 G->D: GROWTH INHIBITED ABOVE 34 C.
DR MUTAGEN 266 G->D: GROWTH INHIBITED ABOVE 34 C.
DR SEQUENCE 297 AA; A94388B4B9CB77FE CRC64;

Query Match 34.7%; Score 43; DB 1; Length 297;
Best Local Similarity 36.8%; Pred. No. 47;
Matches 7; Conservative 6; Mismatches 6; Indels 0;

Qy 1 TANVSSFETPPYVQPYAL 19
:|:|:|:|:|:|
Db 99 SASVNSVQAPHEPYGPLL 117

Search completed: August 17, 2001, 07:37:41
Job time: 19 sec

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 16, 2001, 14:53:49 ; Search time 21.95 Seconds

(without alignments)
126.579 Million cell updates/sec

Title: US-09-428-082-213

Perfect score: 124

Sequence: 1 TANVSSFFWTPYWPYALPL 21

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-----------|--------------------|
| 1 | 55 | 44.4 | 310 | 2 Q9ZHF8 | Q9ZHF8 porphyromon |
| 2 | 49.5 | 39.9 | 509 | 5 O15712 | O15712 paramon |
| 3 | 48 | 38.7 | 525 | 10 Q22630 | Q22630 cucumis mel |
| 4 | 46.5 | 37.5 | 201 | 5 Q22508 | Q22508 caenorhabdi |
| 5 | 46.5 | 37.5 | 352 | 2 Q9FIQ7 | Q9FIQ7 acinetobact |
| 6 | 46 | 37.1 | 425 | 10 Q9FYX3 | Q9FYX3 lycopersico |
| 7 | 46 | 37.1 | 856 | 3 Q74170 | Q74170 aspergillus |
| 8 | 45 | 36.3 | 344 | 5 Q9XW51 | Q9XW51 caenorhabdi |
| 9 | 45 | 36.3 | 432 | 5 Q9NFP2 | Q9NFP2 plasmodium |
| 10 | 45 | 36.3 | 509 | 10 Q43795 | Q43795 nicotiana t |
| 11 | 44.5 | 35.9 | 159 | 5 Q9NME2 | Q9NME2 leishmania |
| 12 | 44 | 35.5 | 57 | 8 Q9TIL8 | Q9TIL8 alaria prae |
| 13 | 44 | 35.5 | 57 | 8 Q9TIL6 | Q9TIL6 alaria cras |
| 14 | 44 | 35.5 | 57 | 8 Q9TIL4 | Q9TIL4 alaria nana |
| 15 | 44 | 35.5 | 57 | 8 Q9TIL2 | Q9TIL2 alaria marg |
| 16 | 44 | 35.5 | 57 | 8 Q9T409 | Q9T409 alaria escu |
| 17 | 44 | 35.5 | 57 | 8 Q9MUK6 | Q9MUK6 alaria gran |
| 18 | 44 | 35.5 | 92 | 14 Q55884 | Q55884 african swi |
| 19 | 44 | 35.5 | 157 | 2 Q49991 | Q49991 mycobacteri |

| | | | | | | |
|----|------|------|-----|----|--------|--------------------|
| 20 | 44 | 35.5 | 161 | 2 | O07200 | O07200 mycobacteri |
| 21 | 44 | 35.5 | 254 | 10 | Q48767 | Q48767 arabidopsis |
| 22 | 44 | 35.5 | 281 | 1 | Q9HK70 | Q9HK70 thermoplas |
| 23 | 44 | 35.5 | 301 | 3 | Q94518 | Q94518 schizosacch |
| 24 | 44 | 35.5 | 334 | 5 | O18104 | O18104 caenorhabdi |
| 25 | 44 | 35.5 | 442 | 10 | Q9LVR2 | Q9LVR2 arabidopsis |
| 26 | 44 | 35.5 | 544 | 3 | Q9HG27 | Q9HG27 schizosacch |
| 27 | 44 | 35.5 | 544 | 5 | Q9I7F2 | Q9I7F2 drosophila |
| 28 | 44 | 35.5 | 596 | 5 | Q9V642 | Q9V642 drosophila |
| 29 | 44 | 35.5 | 618 | 3 | O60134 | O60134 schizosacch |
| 30 | 44 | 35.5 | 632 | 1 | O29768 | O29768 archaeoglob |
| 31 | 44 | 35.5 | 715 | 5 | O61270 | O61270 halocynthia |
| 32 | 44 | 35.5 | 720 | 10 | O81072 | O81072 arabidopsis |
| 33 | 44 | 35.5 | 947 | 14 | Q9E964 | Q9E964 ryegrass mo |
| 34 | 43.5 | 35.1 | 644 | 1 | Q9V057 | Q9V057 pyrococcus |
| 35 | 43 | 34.7 | 61 | 2 | Q52654 | Q52654 rhodosphe |
| 36 | 43 | 34.7 | 154 | 6 | Q9GMX8 | Q9GMX8 macaca fasc |
| 37 | 43 | 34.7 | 166 | 4 | Q9NX18 | Q9NX18 homo sapien |
| 38 | 43 | 34.7 | 182 | 5 | Q9WL94 | Q9WL94 drosophila |
| 39 | 43 | 34.7 | 240 | 10 | Q9SM56 | Q9SM56 psophocarpu |
| 40 | 43 | 34.7 | 354 | 2 | P74242 | P74242 synechocyst |
| 41 | 43 | 34.7 | 422 | 5 | Q9VLZ2 | Q9VLZ2 drosophila |
| 42 | 43 | 34.7 | 437 | 5 | Q9NJP3 | Q9NJP3 caenorhabdi |
| 43 | 43 | 34.7 | 467 | 4 | Q9UJM5 | Q9UJM5 homo sapien |
| 44 | 43 | 34.7 | 531 | 10 | Q42582 | Q42582 arabidopsis |
| 45 | 43 | 34.7 | 531 | 10 | Q9STZ3 | Q9STZ3 arabidopsis |

ALIGNMENTS

RESULT 1

Q9ZHF8

ID Q9ZHF8

AC Q9ZHF8

DT 01-MAY-1999 (TRENBLrel. 10, Created)

DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)

DE 01-MAY-1999 (TRENBLrel. 10, Last annotation update)

DE HYPOTHETICAL 35.6 KDA PROTEIN.

OS Porphyromonas gingivalis (Bacteroides gingivalis).

OC Bacteria; CFB group; Bacteroidaceae; Porphyromonas.

OX NCBI_TaxID=837;

RN [1]

RP SEQUENCE OF 1-54 FROM N.A.

RC STRAIN=W83;

RX MEDLINE=98013087; PubMed=9353038;

RA Fletcher H.M., Morgan R.M., Macrina F.L.;

RT "Nucleotide sequence of the Porphyromonas gingivalis W83 recA homolog

and construction of a recA-deficient mutant.";

RL Infect. Immun. 65:4592-4597(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=W83;

RA Fletcher H.M., Macrina F.L.;

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=W83;

RA Fletcher H.M.;

RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF064682; AAC72889.1;

KW Hypothetical protein.

SQ SEQUENCE 310 AA; 35580 MW; 12979B5284DA56A1 CRC64;

Query Match

Best Local Similarity

Matches 7; Conservative

Score 55; DB 2; Length 310;

63.6%; Pred. No. 2.2;

Mismatches 2; Indels

0; Gaps 0;

Oy 8 EWPYWPY 18

Db 101 DWPYWPY 111

```

RESULT      2
O15712     PRELIMINARY;          PRT;    509 AA.

ID   O15712              AC   O15712;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBurel. 05, Last sequence update)
DE   01-MAR-2001 (TrEMBurel. 16, Last annotation update)
DE   PROTEIN PHOSPHATASE 2B.
OC   Paramesium tetraurelia.
OC   Eukaryote; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC   Paramecium.
NCBI_TaxID=5888;

[1]
SEQUENCE FROM N.A.
STRAIN=51S;
RC RC STRAIN=51S;
RL Russell C.B., Hinrichsen R.D.;
RA Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
CC -I- CATALYTIC ACTIVITY: A PHOSGOPROTEIN + H(2)O -> A PROTEIN +
CC ORTHOPHOSPATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC) (BY
CC SIMILARITY).
CC -I- SIMILARITY: TO SERINE/THREONINE SPECIFIC PROTEIN PHOSPHATASE (OR PPP) FAMILY.
EMLB: AF014922; AAB80918.1. -.
DR HSSP: Q08209; IAU1.
DR InterPro: IPR000934. -.
DR Pfam: PF00149; Stphosphatase; 1.
DR PRINTS: PR00114; STPHSPHTASE.
DR PROSITE: PS00125; SER_THR_PHOSPHATASE; UNKNOWNW_1.
DR SMART: SMO0156; PP2AC; 1.
DR HydroGlas: Iron; Manganese.
SQ SEQUENCE 509 AA; 58552 MW; DBDGE23B113E55A1 CRC64;
```

Query Match 39.9%; Score 49.5; DB 5; Length 509;
Best Local Similarity 45.0%; Pred. No. 23;
Matches 9; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

```
Qy      1 TANVSSFETPYWQPYALP 20
        | | : | : | : | | |
Db     326 TLNIOQFQYTPH---PYLLP 342
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RESULT      3
O22630
ID          O22630      PRELIMINARY;      PRT;      525 AA.
AC          O22630;
DT          01-JAN-1998 (TremBrel. 05, Created)
DT          01-JAN-1998 (TremBrel. 05, Last sequence update)
DT          01-MAY-2000 (TremBrel. 13, Last annotation update)
ADP-GLUCOSE PYROPHOSPHORYLASE LARGE SUBUNIT (EC 2.7.7.27).
MFL1.
Cucumis melo (Muskmelon).
OC          Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sperma
OC          Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euro
OC          Cucurbitales; Cucurbitaceae; Cucumis.
OX          NCBI_TaxID=3656;
ON          [1]
RN          SEQUENCE FROM N.A.
RP          STRAIN=EUNCHRON; TISSUE=FRUIT;
RA          Park S.-W., Kahng H.-Y., Park J.-O., Kim I.-J., chung W.-I.
RL          Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR          EMBL; AF030383; AAB91463.1; -.
DR          Mendel; 26435; Cucme; 2928; 26435.
DR          InterPro; IPR001325; -.
DR          Pfam; PF00483; NTP_transferase; 1.
DR          PROSITE; PS00808; ADP_GLC_PYROPHOSPH_1; UNKNOWN_1.
DR          PROSITE; PS00809; ADP_GLC_PYROPHOSPH_2; 1.
KW          Transferase; Nucleotidyltransferase.
SQ          SEQUENCE      525 AA; 58454 MW; 6CC0EFC3E27925C0 CRC64;

```

Query Match 38.7%; Score 48; DB 10; Length 525;

```

Best Local Similarity 50.08; Pred. No. 39;
Matches 11; Conservative 2; Mismatches 5; Indels 4; Gaps 1;

Qy 3 NVSSFEW-----TPYYWQYPALP 20
    ||| |||      |||: |||
Db 372 NVSEFFYDPKTPFTYSPRFLP 393

RESULT 4
Q22508 PRELIMINARY; PRT; 201 AA.
AC Q22508;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CODED FOR BY C. ELEGANS CDNA YK102C12.3.
GN T14G12.3.
OS Caenorhabditis elegans.
OC Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
OC Rhabditiidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
[1]
RN RP SEQUENCE FROM N.A.
EX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
RA Smalton N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
[2]
RN RN SEQUENCE FROM N.A.
RA Wilcox L.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
[3]
RN RN SEQUENCE FROM N.A.
RP Waterston R.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U41268; AAA82434.1; -.
SQ SEQUENCE 201 AA; 24428 MW; 3802B4733078FC95 CRC64;

Query Match 37.58; Score 46.5; DB 5; Length 201;
Best Local Similarity 41.28; Pred. No. 24;
Matches 7; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

Qy 2 ANVSFFE-WTPYYWQPY 17
    :|: : |||: |||
Db 65 SNIDRYTFYTPFYWQTY 81

RESULT 5
Q9F1Q7 PRELIMINARY; PRT; 352 AA.
AC Q9F1Q7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PUTATIVE TRANSMEMBRANE EFFLUX PROTEIN (FRAGMENT).
OS Acinetobacter sp. M-1.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
NCBI_TaxID=123502;
OX [1]
RN RN SEQUENCE FROM N.A.
RP STRAIN=M-1;
RC

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RX PubMed=11097895;
RA Tani A., Sakai Y., Ishige T., Kato N.;
RT "Thermotable NADP(+) dependent medium-chain alcohol dehydrogenase
from acinetobacter sp. Strain M-1: purification and characterization
and gene expression in escherichia coli.";
RL Appl. Environ. Microbiol. 66:5231-5235(2000).
DR EMBL: AB047854; BAC12274.1; -;
KW Transmembrane.
FT NON_TER 352
SQ SEQUENCE 352 AA; 37004 MW; 6F81C0A996385F97 CRC64;

Query Match 37.5%; Score 46.5; DB 2; Length 352;
Best Local Similarity 44.4%; Pred. No. 42;
Matches 8; Conservative 4; Mismatches 3; Indels 3; Gaps 1;
QY 6 SPFWTPYVW--OPYALP 20
| : : : : : | : : : : : |
199 SHSFPWYHCSQPYLVP 216

RESULT 6
Q9FYX3 PRELIMINARY; PRT; 425 AA.
ID Q9FYX3
AC Q9FYX3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BAC19.3.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asterids I;
OC Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, HEINZ 1706;
RX MEDLINE=20381347; PubMed=10908680;
RA Ku H.-M., Vision T.J., Liu J., Tanksley S.D.;
RT "Comparing sequenced segments of the tomato and Arabidopsis genomes:
Large-scale duplication followed by selective gene loss creates a
network of synteny.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9121-9126(2000).
DR EMBL: AF273333; AAG0118.1; -;
SQ SEQUENCE 425 AA; 46703 MW; CC5130A0A93205D7 CRC64;

Query Match 37.1%; Score 46; DB 10; Length 425;
Best Local Similarity 37.5%; Pred. No. 61;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 3 NVSSFEWTPYVWPYA 18
| : : : : : | : : : : : |
Db 386 NTQLSWPPFPWKPQA 401

RESULT 7
O74170 PRELIMINARY; PRT; 856 AA.
ID O74170
AC O74170;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE AVICELASE III.
GN AVIII.
OS Aspergillus aculeatus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5053;
RN [1]
RP SEQUENCE FROM N.A.
RA Arai M., Takada G., Kawaguchi T., Sumitani J.;
RT "Avicelase III from Aspergillus aculeatus";

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB015511; BAA29031.1; -;
DR HSSP: P00725; 2CBH.
DR InterPro: IPR002860; -;
DR InterPro: IPR002860; -;
DR Pfam: PF00734; CBD_1; 1.
DR Pfam: PF02012; BNR_7;
DR ProDom: PD001821; -; 1.
DR PROSITE: PS00562; CBD_FUNGAL; 1.
DR SMART: SM00236; fCBD; 1.
SQ SEQUENCE 856 AA; 89820 MW; BE085983AF60ED76 CRC64;

Query Match 37.1%; Score 46; DB 3; Length 856;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ANVSSFEWTPYVWQ 15
: : : : : | : : : : : |
Db 182 SNVTSFTWTGTGTFQ 195

RESULT 8
Q9XW51 PRELIMINARY; PRT; 344 AA.
ID Q9XW51
AC Q9XW51;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Y53C10A.6 PROTEIN.
GN Y53C10A.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA White S.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnsough R., Connell M., Copsey T., Cooper J., Coulson A.,
RA Bonfield J., Burton J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Lalster N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
DR EMBL: AL033536; CAA22140.1; -;
SQ SEQUENCE 344 AA; 40061 MW; D37AED6D331D8F78 CRC64;

Query Match 36.3%; Score 45; DB 5; Length 344;
Best Local Similarity 47.6%; Pred. No. 68;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYVWPYALPL 21
| : : : : : | : : : : : |
Db 123 TANVQAEFLPFPKPPATRL 143

RESULT 9
Q9NFP2 PRELIMINARY; PRT; 432 AA.
ID Q9NFP2
AC Q9NFP2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

Matches 8; Conservative 2; Mismatches 5; Indels 2; Gaps 1

Qy 1 TANVSSFETPY--YWQ 15
| | :|||
Db 110 TYNYSDTIWSPGPYWR 126

RESULT 11
Q9NME2 PRELIMINARY; PRT; 159 AA.
ID Q9NME2
AC Q9NME2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 15, Last annotation update)
DE PROBABLE POSSIBLE DYNEIN HEAVY CHAIN, CYTOSOLIC (FRAGMENT).
GN LM26.150.
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxId=5664;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Murphay L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL160493; CAB97768.1;
DR InterPro; IPRO01075; -
DR ProDom; PD002830; -; 1.
FT NON_TER 159 159
SQ SEQUENCE 159 AA; 17519 MW; 0D5329104AF0DB0E CRC64;

Query Match 35.9%; Score 44.5; DB 5; Length 159;
Best Local Similarity 44.4%; Pred. No. 36;
Matches 8; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

Qy 2 ANVSSFEW---TPYWQP 16
| | | | |||:
Db 31 ASVDFAWYQQLRYWEP 48

RESULT 12
Q9TIL8 PRELIMINARY; PRT; 57 AA.
ID Q9TIL8
AC Q9TIL8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN (FRAGMENT).
GN RBCS.
OS Alaria praelonga.
OG Chloroplast.
OC Eukarya; stramenopiles; Phaeophyceae; Laminariales; Alariaceae;
OC Alaria.
OX NCBI_TaxId=88159;
[1]
RN SEQUENCE FROM N.A.
RP Kraan S., Guiry M.D.;
RA "Sexual hybridization experiments and phylogenetic relationships as
inferred from rubisco spacer sequences in the genus Alaria
(Alariaceae, Phaeophyceae).";
RT Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AF109801; AAF21920.1;
DR InterPro; IPRO00894; -
DR InterPro; IPRO02160; -
DR Pfam; PF00101; RuBisCO_small; 1.
DR PROSITE; PS00283; SOYBEAN_KUNITZ; UNKNOWN_1.
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6692 MW; 6F57BIDE4E60E8EC CRC64;

Query Match 35.5%; Score 44; DB 8; Length 57;
Best Local Similarity 45.5%; Pred. No. 15;

Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

QY 6 SFWE--PY----YWPYALPL 21
| | | | | : : : : :
Db 34 SVEWDDPHPRNSYWELWGLPL 55

RESULT 13

Q9TIL6 PRELIMINARY; PRT; 57 AA.
AC Q9TIL6; (Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN (FRAGMENT).
GN RBGS.
OS Alaria crassifolia.
Chloroplast.
Eukaryota; stramenopiles; Phaeophyceae; Laminariales; Alariaceae;
Alaria.

NCBI_TaxID=98220;

SEQUENCE FROM N.A.

Kraan S., Guiry M.D.;

"Sexual hybridization experiments and phylogenetic relationships as inferred from rubisco spacer sequences in the genus Alaria (Alariaceae, Phaeophyceae).";

Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

EMBL; AF109802; AAF21922.1; -

InterPro: IPR000894; -

InterPro: IPR002160; -

Pfam: PF00101; Rubisco_small; 1.

PROSITE; PS00283; SOYBEAN_KUNITZ; UNKNOWN_1.

Chloroplast.

NON_TER 57

SEQUENCE 57 AA; 6692 MW; 6F57B1DE4E60E8EC CRC64;

Query Match

Best Local Similarity 35.5%; Score 44; DB 8; Length 57;

Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

QY 6 SFWE--PY----YWPYALPL 21
| | | | | : : : : :
Db 34 SVEWDDPHPRNSYWELWGLPL 55

RESULT 14

Q9TIL4 PRELIMINARY; PRT; 57 AA.
AC Q9TIL4; (Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN (FRAGMENT).
GN RBGS.
OS Alaria nana.
Chloroplast.
Eukaryota; stramenopiles; Phaeophyceae; Laminariales; Alariaceae;
Alaria.

NCBI_TaxID=98222;

SEQUENCE FROM N.A.

Kraan S., Guiry M.D.;

"Sexual hybridization experiments and phylogenetic relationships as inferred from rubisco spacer sequences in the genus Alaria (Alariaceae, Phaeophyceae).";

Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

EMBL; AF109803; AAF21924.1; -

InterPro: IPR000894; -

InterPro: IPR002160; -

Pfam: PF00101; Rubisco_small; 1.

PROSITE; PS00283; SOYBEAN_KUNITZ; UNKNOWN_1.

KW Chloroplast. 57
SQ SEQUENCE 57 AA; 6692 MW; 6F57B1DE4E60E8EC CRC64;

Query Match 35.5%; Score 44; DB 8; Length 57;
Best Local Similarity 45.5%; Pred. No. 15;
Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

QY 6 SFWE--PY----YWPYALPL 21
| | | | | : : : : :
Db 34 SVEWDDPHPRNSYWELWGLPL 55

RESULT 15

Q9TIL2 PRELIMINARY; PRT; 57 AA.
AC Q9TIL2; (Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN (FRAGMENT).
GN RBGS.
OS Alaria marginata.
Chloroplast.
Eukaryota; stramenopiles; Phaeophyceae; Laminariales; Alariaceae;
Alaria.

NCBI_TaxID=98221;

SEQUENCE FROM N.A.

Kraan S., Guiry M.D.;

"Sexual hybridization experiments and phylogenetic relationships as inferred from rubisco spacer sequences in the genus Alaria (Alariaceae, Phaeophyceae).";

Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

EMBL; AF109804; AAF21926.1; -

InterPro: IPR000894; -

InterPro: IPR002160; -

Pfam: PF00101; Rubisco_small; 1.

PROSITE; PS00283; SOYBEAN_KUNITZ; UNKNOWN_1.

Chloroplast.

NON_TER 57

SEQUENCE 57 AA; 6692 MW; 6F57B1DE4E60E8EC CRC64;

Query Match 35.5%; Score 44; DB 8; Length 57;
Best Local Similarity 45.5%; Pred. No. 15;
Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 2;

QY 6 SFWE--PY----YWPYALPL 21
| | | | | : : : : :
Db 34 SVEWDDPHPRNSYWELWGLPL 55

Search completed: August 16, 2001, 14:56:53
Job time: 184 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 16, 2001, 14:53:49 ; Search time 17.98 Seconds
(without alignments)
70.807 Million cell updates/sec

Title: US-09-428-082-213

Perfect score: 124

Sequence: 1 TANVSFEWYQPYALPL 21

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

11 number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601.*

- 1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
- 7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
- 8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
- 9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
- 10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
- 11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
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- 14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
- 15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
- 16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
- 17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
- 18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
- 19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 124 | 100.0 | 21 | 19 AAW68856 | Peptide binding in |
| 2 | 124 | 100.0 | 21 | 19 AAW58089 | Interleukin-1 type |
| 3 | 124 | 100.0 | 21 | 21 AAB17157 | IL-1 antagonist pe |
| 4 | 114 | 91.9 | 21 | 16 AAR90515 | Interleukin-1 type |
| 5 | 114 | 91.9 | 21 | 18 AAW16208 | Peptide containing |
| 6 | 114 | 91.9 | 21 | 18 AAW15973 | Interleukin-1 type |
| 7 | 114 | 91.9 | 21 | 19 AAW68974 | Peptide binding in |
| 8 | 114 | 91.9 | 21 | 19 AAW68611 | Peptide binding in |
| 9 | 114 | 91.9 | 21 | 19 AAW58116 | Peptide of the inv |
| 10 | 114 | 91.9 | 21 | 20 AAY09703 | Interleukin-1 type |
| 11 | 114 | 91.9 | 21 | 21 AAB17757 | IL-1 antagonist pe |

| | | | | | |
|----|------|------|-----|-------------|--------------------|
| 12 | 114 | 91.9 | 21 | 21 AAB17794 | IL-1 antagonist pe |
| 13 | 114 | 91.9 | 21 | 21 AAB17814 | IL-1 antagonist pe |
| 14 | 114 | 91.9 | 21 | 21 AAB17899 | IL-1 antagonist pe |
| 15 | 114 | 91.9 | 21 | 21 AAB17913 | IL-1 antagonist pe |
| 16 | 87 | 70.2 | 15 | 16 AAR90521 | Interleukin-1 type |
| 17 | 87 | 70.2 | 15 | 18 AAW15855 | Interleukin-1 type |
| 18 | 87 | 70.2 | 15 | 18 AAW15967 | Interleukin-1 type |
| 19 | 87 | 70.2 | 15 | 19 AAW68931 | Peptide binding in |
| 20 | 87 | 70.2 | 15 | 19 AAW58078 | Interleukin-1 type |
| 21 | 87 | 70.2 | 15 | 20 AAY09695 | Interleukin-1 type |
| 22 | 87 | 70.2 | 15 | 21 AAB17201 | IL-1 antagonist pe |
| 23 | 87 | 70.2 | 15 | 21 AAB17795 | IL-1 antagonist pe |
| 24 | 87 | 70.2 | 15 | 21 AAB17807 | IL-1 antagonist pe |
| 25 | 87 | 70.2 | 15 | 21 AAB17820 | IL-1 antagonist pe |
| 26 | 87 | 70.2 | 17 | 19 AAW68957 | Peptide binding in |
| 27 | 87 | 70.2 | 17 | 19 AAW58118 | Peptide of the inv |
| 28 | 87 | 70.2 | 17 | 20 AAV10070 | Interleukin-1 type |
| 29 | 87 | 70.2 | 19 | 21 AAB17901 | IL-1 antagonist pe |
| 30 | 87 | 70.2 | 21 | 21 AAB17943 | IL-1 R antagonist |
| 31 | 87 | 70.2 | 21 | 21 AAB17944 | IL-1 R antagonist |
| 32 | 87 | 70.2 | 248 | 21 AAB17953 | Fc-IL-1 antagonist |
| 33 | 87 | 70.2 | 248 | 21 AAB17954 | IL-1 antagonist-Fc |
| 34 | 78.5 | 63.3 | 21 | 18 AAW16242 | Peptide containing |
| 35 | 78.5 | 63.3 | 21 | 19 AAW68876 | Peptide binding in |
| 36 | 78.5 | 63.3 | 21 | 19 AAW58358 | IL-1RTI binding pe |
| 37 | 78.5 | 63.3 | 21 | 20 AAB10009 | Interleukin-1 type |
| 38 | 78.5 | 63.3 | 21 | 21 AAB17791 | IL-1 antagonist pe |
| 39 | 78 | 62.9 | 15 | 16 AAR90523 | Interleukin-1 type |
| 40 | 78 | 62.9 | 15 | 16 AAR90522 | Interleukin-1 type |
| 41 | 78 | 62.9 | 15 | 18 AAW15968 | Interleukin-1 type |
| 42 | 78 | 62.9 | 15 | 18 AAW15971 | Interleukin-1 type |
| 43 | 78 | 62.9 | 15 | 19 AAW69003 | Peptide binding in |
| 44 | 78 | 62.9 | 15 | 19 AAW68956 | Peptide binding in |
| 45 | 78 | 62.9 | 15 | 19 AAW58079 | Interleukin-1 type |

ALIGNMENTS

| | |
|----------|---|
| RESULT | 1 |
| AAW68856 | |
| ID | AAW68856 standard; peptide; 21 AA. |
| XX | |
| AC | AAW68856; |
| XX | |
| DT | 01-OCT-1998 (first entry) |
| XX | |
| DE | Peptide binding interleukin-1 type I receptor. |
| XX | |
| KW | Antagonist; interleukin-1; IL-1; IL-1 type I receptor; IL-1RTI; |
| KW | treatment; IL-1 disorder. |
| XX | |
| OS | Synthetic |
| XX | |
| PN | US5786331-A. |
| XX | |
| PD | 28-JUL-1998. |
| XX | |
| PF | 05-JUN-1995; 95US-0465391. |
| XX | |
| PR | 05-JUN-1995; 95US-0465391. |
| PR | 02-FEB-1994; 94US-0190788. |
| PR | 01-FEB-1995; 95US-0383474. |
| XX | |
| PA | (AFFY-) AFFYMAX TECHNOLOGIES NV. |
| PA | (HMRI) HOECHST MARION ROUSSEL INC. |
| XX | |
| PI | Baldwin D, Barrett RW, Bovy PR, Jacobs JW, Leahy EM; |
| PI | Pottorf RS, Yanofsky SD; |
| XX | |
| DR | WPI; 1998-436582/37. |
| XX | |
| PT | Antagonisation of action of interleukin-1 on type I receptor - by |

CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linker; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytosolic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAG69443
 CC to AAG69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 21 AA;

Query Match 100.0%; Score 124; DB 21; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0;
 QY 1 TANVSSFEWTPYWPYALPL 21
 ||||| ||||| ||||| |||||
 Db 1 tanvssfewtpyywqpyalpl 21

RESULT 4
 ID AAR90515
 XX AAR90515 standard; peptide; 21 AA.
 AC AAR90515;
 XX
 DT 14-MAR-1996 (first entry)
 XX
 DE Interleukin-1 type I receptor binding peptide #1.
 DE
 KW Interleukin-1 type I receptor; IL-1; IL-1RTI; atherosclerosis;
 KW rheumatoid arthritis; osteoporosis; HIV; AIDS; bacterial infection;
 KW respiratory distress syndrome; acute myelogenous leukaemia;
 KW coal miner pneumococcus; alcoholic cirrhosis; cuprophane haemodialysis;
 KW cardiopulmonary bypass; chronic hepatitis B; thermal injury;
 KW reticulohistiocytosis; sarcoidosis; tuberculosis; obstructive jaundice;
 KW Paget's disease; osteomalacia; IDDM; Kawasaki's disease;
 KW inflammatory bowel disease; sepsis; toxic shock; luteal phase; therapy.
 XX
 OS Synthetic.
 XX
 Key Location/Qualifiers
 Region 13..20
 /note= "core sequence #1"
 XX
 PN W09520973-A1.
 XX
 PD 10-AUG-1995.
 XX
 PF 01-FEB-1995; 95WO-US01590.
 XX
 PR 02-FEB-1994; 94US-0190788.
 XX
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX
 PI Baldwin D, Barrett RW, Jacobs JW, Yanofsky SD;
 XX
 DR WPI; 1995-283605/37.
 XX
 PT Interleukin-1 type I receptor binding compounds - used e.g. in the
 PT treatment of osteoporosis, HIV and hepatitis B
 XX
 PS Claim 22; Page 53; 56pp; English.
 XX
 CC The sequences represented by R09515-AAR90527 are interleukin-1 type I
 CC receptor (IL-1RTI) binding peptides. These peptides contain the core
 CC sequence represented by AAR83759. These sequences block the binding of

CC IL-1 to IL-1RTI. The sequences were synthesised by using solid phase
 CC synthesis. These sequences are useful in vitro for studying the IL-1
 CC receptor binding process, for developing and assaying other compounds
 CC which bind to the receptor, and for measuring the expression of IL-1RTI
 CC on cell surfaces. They can also be used to monitor the effectiveness of
 CC treatments which influence IL-1 production. They could also be used for
 CC treating disorders which are susceptible to treatment with an IL-1
 CC inhibitor, e.g. atherosclerosis, rheumatoid arthritis, osteoporosis,
 CC HIV, AIDS, bacterial infection, respiratory distress syndrome, acute
 CC myelogenous leukaemia, coal miner pneumococcus, graft vs. host disease,
 CC alcoholic cirrhosis, cuprophane haemodialysis, cardiopulmonary bypass,
 CC chronic hepatitis B, thermal injury, reticulohistiocytosis, sarcoidosis,
 CC tuberculosis, obstructive jaundice, Paget's disease, osteomalacia, IDDM,
 CC Kawasaki's disease, inflammatory bowel disease, sepsis, toxic shock and
 CC luteal phase. These compounds may also be conjugated so that they act
 CC as antagonists, or agonists, of IL-1RTI and may be used to direct a
 CC cytotoxic or therapeutic agent to a cell expressing this receptor.
 XX
 SQ Sequence 21 AA;

Query Match 91.9%; Score 114; DB 16; Length 21;
 Best Local Similarity 95.2%; Pred. No. 3.9e-11;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYWPYALPL 21
 ||||| ||||| ||||| |||||
 Db 1 tanvssfewtpyywqpyalpl 21

RESULT 5
 ID AAW16208
 XX AAW16208 standard; peptide; 21 AA.
 AC AAW16208;
 XX
 DT 19-AUG-1997 (first entry)
 XX
 DE Peptide containing QPY or QPY-like motif.
 DE
 KW Interleukin-1; type I receptor; IL-1RTI; agonist; antagonist.
 XX
 OS Synthetic.
 XX
 PN W09639165-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 05-JUN-1996; 96WO-US09835.
 XX
 PR 05-JUN-1995; 95US-0464538.
 XX
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX
 PI Baldwin D, Barrett RW, Bovy PR, Dharanipragada R;
 PI Jacobs JW, Leahy EM, Pottorf RS, Tomlinson RC, Yanofsky SD;
 XX
 DR WPI; 1997-042846/04.
 XX
 PT Interleukin-1 type I receptor inhibitor peptide(s) and compounds -
 PT used to antagonise the activity of IL-1, for treatment of e.g. AIDS,
 PT rheumatoid arthritis, chronic hepatitis B, etc.
 XX
 PS Disclosure; Page 32; 74pp; English.
 XX
 CC The invention relates to peptides which bind to the IL-1 type I
 CC receptor and which comprise the motif WXXG-Z1-W or the motif
 CC XXQ-Z5-V-Z6-XX, in which X can be any one of the 20 genetically
 CC coded L-amino acids or the stereoisomeric D-amino acids or
 CC unnatural amino acids; Z1 is L, I, A or Q; Z5 is P or azetidine
 CC (presumably intended to be azetidine carboxylic acid); and Z6 is S,
 CC A, V or L.
 CC The present sequence is that of a random peptide from a library of

CC peptides containing the "XXQ-25-Y-26-XX" motif, the library being
 CC constructed to screen the peptides for activity.
 CC IL-1 type I receptor-binding peptides may be useful in the treatment
 CC of a variety of IL-1 related disorders including atherosclerosis,
 CC rheumatoid arthritis, osteoporosis, HIV infection and AIDS, bacterial
 CC infection, respiratory distress syndrome, acute myelogenous leukaemia,
 CC graft versus host disease, coal miner pneumoconiosis, alcoholic
 CC cirrhosis, cuprophane haemodialysis, cardiopulmonary bypass, chronic
 CC hepatitis B, tuberculosis, obstructive jaundice, Paget's disease and
 CC osteomalacia, IDDM, Kawasaki's disease, inflammatory bowel disease,
 CC sepsis, toxic shock and luteal phase.

XX Sequence 21 AA;

Query Match 91.9%; Score 114; DB 18; Length 21;
 Best Local Similarity 95.2%; Pred. No. 3.9e-11;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TANVSSFETPYWQPYALPL 21
 ||||| ||||| ||||| |||||
 Db 1 tanvssfewtpgywqpyalpl 21

RESULT 6

AAW15973
 ID AAW15973 standard; peptide; 21 AA.

AC AAW15973;

XX 19-AUG-1997 (first entry)

XX Interleukin-1 type I receptor binding peptide.

XX IL-1RtI; agonist; antagonist.

OS Synthetic.

PN WO9639165-A1.

XX 12-DEC-1996.

XX 05-JUN-1996; 95WO-US09835.

XX 05-JUN-1995; 95US-0464538.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX Baldwin D, Barrett RW, Bovy PR, Dharanipragada R;
 XX Jacobs JW, Leahy EM, Pottorf RS, Tomlinson RC, Yanofsky SD;

DR WPI; 1997-042846/04.

XX Interleukin-1 type I receptor inhibitor peptide(s) and compounds -
 PT used to antagonise the activity of IL-1, for treatment of e.g. AIDS,
 PT rheumatoid arthritis, chronic hepatitis B, etc.

PS Disclosure; Page 5; 74pp; English.

XX The patent discloses, inter alia, peptides of 8-40 amino acids
 CC in length which bind to the IL-1 type I receptor and which comprise
 CC a core sequence of formula XXQ-25-Y-26-XX, in which X can be any
 CC one of the 20 genetically coded L-amino acids or the stereoisomeric
 CC D-amino acids or unnatural amino acids: 25 is P or azetidine (presumably
 CC intended to be azetidine carboxylic acid); and 26 is S, A, V or L.
 CC These peptides may be used in the treatment of a variety of IL-1
 CC related disorders including atherosclerosis, rheumatoid arthritis,
 CC osteoporosis, HIV infection and AIDS, bacterial infection, respiratory
 CC distress syndrome, acute myelogenous leukaemia, graft versus host
 CC disease, coal miner pneumoconiosis, alcoholic cirrhosis, cuprophane
 CC haemodialysis, cardiopulmonary bypass, chronic hepatitis B,
 CC tuberculosis, obstructive jaundice, Paget's disease and osteomalacia,
 CC IDDM, Kawasaki's disease, inflammatory bowel disease, sepsis, toxic

CC shock and luteal phase.
 CC the present sequence is an especially preferred peptide containing
 CC the above motif.

XX Sequence 21 AA;

Query Match 91.9%; Score 114; DB 18; Length 21;
 Best Local Similarity 95.2%; Pred. No. 3.9e-11;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TANVSSFETPYWQPYALPL 21
 ||||| ||||| ||||| |||||
 Db 1 tanvssfewtpgywqpyalpl 21

RESULT 7

AAW68974
 ID AAW68974 standard; peptide; 21 AA.

AC AAW68974;

XX 01-OCT-1998 (first entry)

XX Peptide binding Interleukin-1 type I receptor.

XX Antagonist; interleukin-1; IL-1; IL-1 type I receptor; IL-1RtI;
 KW treatment; IL-1 disorder.

XX Synthetic.

XX US5786331-A.

XX 28-JUL-1998.

XX 05-JUN-1995; 95US-0465391.

XX 05-JUN-1995; 95US-0465391.

XX 02-FEB-1994; 94US-0190788.

XX 01-FEB-1995; 95US-0383474.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX (HMRI) HOECHST MARION ROUSSEL INC.

XX Baldwin D, Barrett RW, Bovy PR, Jacobs JW, Leahy EM;
 XX Pottorf RS, Yanofsky SD;

XX WPI; 1998-436582/37.

XX Antagonisation of action of interleukin-1 on type I receptor - by
 PT contacting receptor with selected peptides

XX Disclosure; Columns 215-216; 118pp; English.

XX AAW68970-82 represent peptide sequences which antagonise the action of
 CC interleukin-1 (IL-1) by binding to an IL-1 type I receptor (IL-1RtI).
 CC The peptides are used in the treatment of disorders mediated by IL-1,
 CC e.g. atherosclerosis, arthritis, osteoporosis, AIDS, bacterial
 CC infections, respiratory distress syndrome, acute myelogenous
 CC leukaemia, graft-versus-host disease, pneumoconiosis, cirrhosis,
 CC cuprophane haemodialysis, cardiopulmonary bypass, hepatitis B, thermal
 CC injury, reticulohistiocytosis, sarcoidosis, tuberculosis, obstructive
 CC jaundice, Paget's disease, osteomalacia, diabetes, Kawasaki's disease,
 CC inflammatory bowel disease, sepsis, toxic shock and luteal phase.

XX Sequence 21 AA;

Query Match 91.9%; Score 114; DB 19; Length 21;
 Best Local Similarity 95.2%; Pred. No. 3.9e-11;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TANVSSFETPYWQPYALPL 21

Db 1 tanvssfewtpgywqpyalpl 21

RESULT 8
AAW68611
ID AAW68611 standard; peptide; 21 AA.
XX AC AAW68611;
XX
DT 01-OCT-1998 (first entry)
XX
XX Peptide binding interleukin-1 type I receptor.
DE
XX Antagonist; interleukin-1; IL-1; IL-1 type I receptor; IL-1rtI;
KW treatment; IL-1 disorder.
KW
XX
XX Synthetic.
OS
XX US5786331-A.
XX
PD 28-JUL-1998.
XX
XX 05-JUN-1995; 95US-0465391.
XX
XX 05-JUN-1995; 95US-0465391.
PR 02-FEB-1994; 94US-0190788.
PR 01-FEB-1995; 95US-0383474.
XX
XX (AFFY-) AFFYMAX TECHNOLOGIES NV.
PA (HMRI) HOECHST MARION ROUSSEL INC.
PA
XX
XX Baldwin D, Barrett RW, Bovy PR, Jacobs JW, Leahy EM;
PI Pottorf RS, Yanofsky SD;
PI
XX
XX WPI; 1998-436582/37.
DR
XX
XX Antagonisation of action of interleukin-1 on type I receptor - by
PT contacting receptor with selected peptides
PT
XX
PS Disclosure; Column 3; 118pp; English.
XX
XX Peptides AAW68611-16 represent peptides that antagonise the action of
CC interleukin-1 (IL-1) by binding to an IL-1 type I receptor (IL-1rtI).
CC The peptides are used in the treatment of disorders mediated by
CC IL-1, e.g. atherosclerosis, arthritis, osteoporosis, AIDS, bacterial
CC infections, respiratory distress syndrome, acute myelogenous leukaemia,
CC graft-versus-host disease, pneumoconiosis, cirrhosis, cuprophane
CC haemodialysis, cardiopulmonary bypass, hepatitis B, thermal injury,
CC reticulohistiocytosis, sarcoidosis, tuberculosis, obstructive jaundice,
CC Paget's disease, osteomalacia, diabetes, Kawasaki's disease,
CC inflammatory bowel disease, sepsis, toxic shock and luteal phase.
XX
XX Sequence 21 AA;
SQ

Query Match 91.98; Score 114; DB 19; Length 21;
Best Local Similarity 95.28; Pred. No. 3.9e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPGYWQPYALPL 21
XXXXXXXXXXXXXXXXXXXX
Db 1 tanvssfewtpgywqpyalpl 21

RESULT 9
AAW58116
ID AAW58116 standard; peptide; 21 AA.
XX AC AAW58116;
XX
DT 14-AUG-1998 (first entry)
XX

XX Interleukin-1 type I receptor; IL-1RtI; inflammatory bowel disease;
 KW rheumatoid arthritis; osteoarthritis; psoriasis; encephalitis;
 KW glomerulonephritis; respiratory distress syndrome.
 XX Synthetic.
 OS
 PN US5880096-A.
 XX
 XX 09-MAR-1999.
 PD
 XX
 XX 05-JUN-1995; 35US-0463076.
 PF
 XX
 XX 05-JUN-1995; 35US-0463076.
 PR
 XX 02-FEB-1994; 94US-0190788.
 PR
 XX 01-FEB-1995; 95US-0383474.
 PR
 XX (AFFY-) AFFYMAX TECHNOLOGIES NV.
 PA
 XX Barrett RW, Yanofsky SD;
 PI
 XX WPI; 1999-204004/17.
 PS
 XX New peptides which bind to the interleukin-1 type I receptor
 PT (IL-1RtI) - useful for the study of IL-1RtI mediated activities and
 PT the treatment/prevention of diseases with an inappropriate
 PT production or response to interleukin-1
 XX
 XX Disclosure; Column 3; 120pp; English.
 XX
 CC The invention relates to new peptides which bind to the
 CC interleukin-1 type I receptor (IL-1RtI). These include 'lead'
 CC peptides identified using random peptide diversity generating
 CC systems (e.g. 'peptides on phage' and 'peptides on plasmids'
 CC systems) and derivatives of the 'lead' peptides which have a
 CC similar structure or shape as the lead compounds but which differ
 CC with respect to susceptibility to hydrolysis or proteolysis and/or
 CC with respect to biological properties.
 CC These peptides are useful as agonists/antagonists for the study of
 CC IL-1RtI mediated activities (e.g. as labels and probes), for the
 CC identification of new IL-1 receptor blockers, and for the
 CC identification, diagnosis and treatment/prevention of diseases with
 CC an inappropriate production or response to IL-1, e.g. rheumatoid
 CC arthritis, osteoarthritis, psoriasis, inflammatory bowel disease,
 CC encephalitis, glomerulonephritis, and respiratory distress syndrome.
 XX
 XX Sequence 21 AA;

Query Match 91.9%; Score 114; DB 20; Length 21;
 Best Local Similarity 95.2%; Pred. No. 3.9e-11;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TANVSSFEWTPYWPYALPL 21
 ||||||||| |||||||||
 Db 1 tanvssfewtpgywqypalpl 21

RESULT 11
 AAB17757
 ID AAB17757 standard; Peptide; 21 AA.
 XX
 XX AAB17757;
 AC
 XX 31-OCT-2000 (first entry)
 DT
 XX IL-1 antagonist peptide sequence SEQ ID NO: 861.
 DE
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mmetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;

KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX Synthetic.
 OS
 PN WO200024782-A2.
 XX
 XX 04-MAY-2000.
 PD
 XX 25-OCT-1999; 99WO-US25044.
 PF
 XX 23-OCT-1998; 98US-0105371.
 PR
 XX 22-OCT-1999; 99US-0428082.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 XX Feige U, Liu C, Cheetham J, Boone TC;
 PI
 XX WPI; 2000-350702/30.
 DR
 XX Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases.
 PT
 XX Claim 10; Page 490; 608pp; English.
 PS
 XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P*3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX
 XX Sequence 21 AA;

Query Match 91.9%; Score 114; DB 21; Length 21;
 Best Local Similarity 95.2%; Pred. No. 3.9e-11;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TANVSSFEWTPYWPYALPL 21
 ||||||||| |||||||||
 Db 1 tanvssfewtpgywqypalpl 21

RESULT 12
 AAB17794
 ID AAB17794 standard; Peptide; 21 AA.
 XX
 XX AAB17794;
 AC
 XX 31-OCT-2000 (first entry)
 DT
 XX IL-1 antagonist peptide sequence SEQ ID NO: 898.
 DE
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mmetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;

KW asthma; thrombosis; pharmaceutical.

XX Synthetic.

XX WO200024782-A2.

XX 04-MAY-2000.

XX 25-OCT-1999; 99WO-US25044.

XX 23-OCT-1998; 98US-0105371.

XX 22-OCT-1999; 99US-0428082.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham J, Boone TC;

XX WPI; 2000-350702/30.

XX Novel composition of matter comprising an Fc domain and
pharmacologically active peptides, useful for treating cancer and
autoimmune diseases.

XX Claim 10; Page 504; 608pp; English.

XX The present invention describes composition of matter (I) comprising an
Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
-(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

XX where P1, P2, P3, and P4 = are each independently sequences of
pharmacologically active peptides; L1, L2, L3, and L4 = are each
independently linkers; and a, b, c, d, e, and f = are each independently
0 or 1, provided that at least 1 of a and b is 1. The composition can
have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
activities. DNAs, vectors and host cells from the present invention can
be used for producing pharmaceutical compositions. The compositions are
useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
The use of an Fc domain (rather than a Fab domain) can provide a longer
half-life or incorporate functions such as Fc receptor binding, protein
A binding, complement fixation, and possibly placental transfer. AAA69443
to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
sequences used in the exemplification of the present invention.

XX Sequence 21 AA;

Query Match 91.9%; Score 114; DB 21; Length 21;

Best Local Similarity 95.2%; Pred. No. 3.9e-11;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TANVSSFETPYWQPYALPL 21

Db 1 tanvssfetpywqpyalpl 21

RESULT 13

AAB17814

ID AAB17814 standard; Peptide; 21 AA.

XX AAB17814;

XX 31-OCT-2000 (first entry)

XX IL-1 antagonist peptide sequence SEQ ID NO:918.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase;
asthma; thrombosis; pharmaceutical.

XX OS

XX Synthetic.

XX WO200024782-A2.

XX 04-MAY-2000.

XX 25-OCT-1999; 99WO-US25044.

XX 23-OCT-1998; 98US-0105371.

XX 22-OCT-1999; 99US-0428082.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham J, Boone TC;

XX WPI; 2000-350702/30.

XX Novel composition of matter comprising an Fc domain and
pharmacologically active peptides, useful for treating cancer and
autoimmune diseases.

XX Claim 10; Page 514; 608pp; English.

XX The present invention describes composition of matter (I) comprising an
Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
-(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
XX where P1, P2, P3, and P4 = are each independently sequences of
pharmacologically active peptides; L1, L2, L3, and L4 = are each
independently linkers; and a, b, c, d, e, and f = are each independently
0 or 1, provided that at least 1 of a and b is 1. The composition can
have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
activities. DNAs, vectors and host cells from the present invention can
be used for producing pharmaceutical compositions. The compositions are
useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
The use of an Fc domain (rather than a Fab domain) can provide a longer
half-life or incorporate functions such as Fc receptor binding, protein
A binding, complement fixation, and possibly placental transfer. AAA69443
to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
sequences used in the exemplification of the present invention.

XX Sequence 21 AA;

Query Match 91.9%; Score 114; DB 21; Length 21;

Best Local Similarity 95.2%; Pred. No. 3.9e-11;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TANVSSFETPYWQPYALPL 21

Db 1 tanvssfetpywqpyalpl 21

RESULT 14

AAB17899

ID AAB17899 standard; Peptide; 21 AA.

XX AAB17899;

XX 31-OCT-2000 (first entry)

XX IL-1 antagonist peptide sequence SEQ ID NO:1003.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase;
asthma; thrombosis; pharmaceutical.

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OM protein - protein search, using sw model

Run on: August 16, 2001, 14:53:49 ; Search time 12.18 seconds
(without alignments)
35.501 Million cell updates/sec

Title: US-09-428-082-213
Perfect score: 124
Sequence: 1 TANVSSFEWTPYWPYALPL 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 124 | 100.0 | 21 | 1 | US-08-190-788A-11 |
| 2 | 124 | 100.0 | 21 | 1 | US-08-190-788A-256 |
| 3 | 124 | 100.0 | 21 | 1 | US-08-465-391A-256 |
| 4 | 124 | 100.0 | 21 | 2 | US-08-464-538B-256 |
| 5 | 114 | 91.9 | 21 | 1 | US-08-383-474B-17 |
| 6 | 114 | 91.9 | 21 | 1 | US-08-465-391A-11 |
| 7 | 114 | 91.9 | 21 | 1 | US-08-465-391A-374 |
| 8 | 114 | 91.9 | 21 | 2 | US-08-464-538B-11 |
| 9 | 114 | 91.9 | 21 | 2 | US-08-464-538B-371 |
| 10 | 114 | 91.9 | 21 | 2 | US-08-463-076E-20 |
| 11 | 87 | 70.2 | 15 | 1 | US-08-383-474B-10 |
| 12 | 87 | 70.2 | 15 | 1 | US-08-465-391A-331 |
| 13 | 87 | 70.2 | 15 | 2 | US-08-464-538B-329 |
| 14 | 87 | 70.2 | 15 | 2 | US-08-463-076E-12 |
| 15 | 87 | 70.2 | 17 | 1 | US-08-383-474B-300 |
| 16 | 87 | 70.2 | 17 | 1 | US-08-465-391A-357 |
| 17 | 87 | 70.2 | 17 | 2 | US-08-464-538B-354 |
| 18 | 87 | 70.2 | 17 | 2 | US-08-463-076E-391 |
| 19 | 78.5 | 63.3 | 21 | 1 | US-08-190-788A-276 |
| 20 | 78.5 | 63.3 | 21 | 1 | US-08-383-474B-279 |
| 21 | 78.5 | 63.3 | 21 | 1 | US-08-465-391A-276 |
| 22 | 78.5 | 63.3 | 21 | 2 | US-08-464-538B-276 |
| 23 | 78.5 | 63.3 | 21 | 2 | US-08-463-076E-330 |
| 24 | 78 | 62.9 | 15 | 1 | US-08-383-474B-11 |
| 25 | 78 | 62.9 | 15 | 1 | US-08-383-474B-14 |
| 26 | 78 | 62.9 | 15 | 1 | US-08-465-391A-356 |
| 27 | 78 | 62.9 | 15 | 1 | US-08-465-391A-403 |

| | | | | | | |
|----|----|------|----|---|--------------------|-------------------|
| 28 | 78 | 62.9 | 15 | 2 | US-08-464-538B-353 | Sequence 353, App |
| 29 | 78 | 62.9 | 15 | 2 | US-08-464-538B-400 | Sequence 400, App |
| 30 | 78 | 62.9 | 15 | 2 | US-08-463-076E-13 | Sequence 13, Appl |
| 31 | 78 | 62.9 | 15 | 2 | US-08-463-076E-16 | Sequence 16, Appl |
| 32 | 76 | 61.3 | 21 | 1 | US-08-190-788A-248 | Sequence 248, App |
| 33 | 76 | 61.3 | 21 | 1 | US-08-383-474B-251 | Sequence 251, App |
| 34 | 76 | 61.3 | 21 | 1 | US-08-465-391A-248 | Sequence 248, App |
| 35 | 76 | 61.3 | 21 | 2 | US-08-464-538B-248 | Sequence 248, App |
| 36 | 76 | 61.3 | 21 | 2 | US-08-463-076E-305 | Sequence 305, App |
| 37 | 75 | 60.5 | 21 | 1 | US-08-190-788A-246 | Sequence 246, App |
| 38 | 75 | 60.5 | 21 | 1 | US-08-383-474B-249 | Sequence 249, App |
| 39 | 75 | 60.5 | 21 | 1 | US-08-465-391A-246 | Sequence 246, App |
| 40 | 75 | 60.5 | 21 | 2 | US-08-464-538B-246 | Sequence 246, App |
| 41 | 75 | 60.5 | 21 | 2 | US-08-463-076E-303 | Sequence 303, App |
| 42 | 73 | 58.9 | 15 | 1 | US-08-383-474B-12 | Sequence 12, Appl |
| 43 | 73 | 58.9 | 15 | 1 | US-08-465-391A-402 | Sequence 402, App |
| 44 | 73 | 58.9 | 15 | 2 | US-08-464-538B-399 | Sequence 399, App |
| 45 | 73 | 58.9 | 15 | 2 | US-08-463-076E-14 | Sequence 14, Appl |

ALIGNMENTS

RESULT 1
US-08-190-788A-11
; Sequence 11, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190.788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-190-788A-11

Query Match 100.0%; Score 124; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYWPYALPL 21
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Db 1 TANVSSFEWTPYWPYALPL 21

RESULT 2

US-08-190-788A-256
; Sequence 256, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yancofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David W.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190.788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 256:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-190-788A-256

Query Match 100.0%; Score 124; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYWPYALPL 21
|||||
Db 1 TANVSSFEWTPYWPYALPL 21

RESULT 3

US-08-465-391A-256
; Sequence 256, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yancofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

Query Match 100.0%; Score 124; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYWPYALPL 21
|||||
Db 1 TANVSSFEWTPYWPYALPL 21

RESULT 4

US-08-464-538B-256
; Sequence 256, Application US/08464538B
; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yancofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

Query Match 100.0%; Score 124; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYWPYALPL 21
|||||
Db 1 TANVSSFEWTPYWPYALPL 21

RESULT 5

US-08-465-391A-256
; Sequence 256, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yancofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

APPLICANT: Bovy, Phillippe R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 405
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,391A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5786331v1el, Vern
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 256:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-391A-256

Query Match 100.0%; Score 124; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYWPYALPL 21
|||||
Db 1 TANVSSFEWTPYWPYALPL 21

US-08-464-538B-256
; Sequence 256, Application US/08464538B
; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yancofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

Query Match 100.0%; Score 124; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYWPYALPL 21
|||||
Db 1 TANVSSFEWTPYWPYALPL 21

US-08-465-391A-256
; Sequence 256, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yancofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

Query Match 100.0%; Score 124; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYWPYALPL 21
|||||
Db 1 TANVSSFEWTPYWPYALPL 21

US-08-464-538B-256
; Sequence 256, Application US/08464538B
; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yancofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

Query Match 100.0%; Score 124; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TANVSSFEWTPYWPYALPL 21
|||||
Db 1 TANVSSFEWTPYWPYALPL 21

US-08-465-391A-256
; Sequence 256, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yancofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

Query Match 100.0%; Score 124; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,538B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528A-001810
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 256:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-538B-256

Query Match 100.0%; Score 124; DB 2; Length 21;
Best Local Similarity 100.0%; Pred No. 1.5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 TANVSSFEWTPYYWQYALPL 21
Db 1 TANVSSFEWTPYYWQYALPL 21

RESULT 5
US-08-383-474B-17
Sequence 17, Application US/08383474B
Patent No. 5767234
GENERAL INFORMATION:
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Barrett, Ronald W.
APPLICANT: Baldwin, David N.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: the IL-1 Receptor
NUMBER OF SEQUENCES: 314
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend & Townsend & Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/383,474B
FILING DATE: 01-FEB-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-383-474B-17

Query Match 91.9%; Score 114; DB 1; Length 21;
Best Local Similarity 95.2%; Pred No. 4.5e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 TANVSSFEWTPYYWQYALPL 21
Db 1 TANVSSFEWTPYYWQYALPL 21

RESULT 6
US-08-465-391A-11
Sequence 11, Application US/08465391A
Patent No. 5786331
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Philippe R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 405
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,391A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: No. 5786331vi1, Vern
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-391A-11

Query Match 91.9%; Score 114; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.5e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TANVSSFEWTPYWPYALPL 21
|||||
1 TANVSSFEWTPYWPYALPL 21

RESULT 7
US-08-465-391A-374
Sequence 374, Application US/08465391A
Patent No. 5786331
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Philippe R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
NUMBER OF SEQUENCES: 405
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,391A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5786331vi1, Vern
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-391A-11

NAME: No. 5786331vi1, Vern
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-391A-374

Query Match 91.9%; Score 114; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.5e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TANVSSFEWTPYWPYALPL 21
|||||
1 TANVSSFEWTPYWPYALPL 21

RESULT 8
US-08-464-538B-11
Sequence 11, Application US/08464538B
Patent No. 5861476
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Philippe R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
NUMBER OF SEQUENCES: 402
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,538B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528A-001810
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-538B-11

Query Match 91.9%; Score 114; DB 2; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.5e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TANVSSFEWTPYQWQYALPL 21
|||||
Db 1 TANVSSFEWTPGYWQYALPL 21

RESULT 9

US-08-464-538B-371
; Sequence 371, Application US/08464538B
; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leamy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,538B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528A-001810
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 371:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-538B-371

Query Match 91.9%; Score 114; DB 2; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.5e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TANVSSFEWTPYQWQYALPL 21
|||||
Db 1 TANVSSFEWTPGYWQYALPL 21

RESULT 10

US-08-463-076E-20
; Sequence 20, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,076E
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Snyder, Joseph R.
REGISTRATION NUMBER: 39,381
REFERENCE/DOCKET NUMBER: 16528A-0018500S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-076E-20

Query Match 91.9%; Score 114; DB 2; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.5e-11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TANVSSFEWTPYQWQYALPL 21
|||||
Db 1 TANVSSFEWTPGYWQYALPL 21

RESULT 11

US-08-383-474B-10
; Sequence 10, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,474B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Snyder, Joseph R.
REGISTRATION NUMBER: 39,381
REFERENCE/DOCKET NUMBER: 16528A-0018500S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-076E-20

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/383,474B
;; FILING DATE: 01-FEB-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/190,788
;; FILING DATE: 02-FEB-1994
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stevens, Lauren L.
;; REGISTRATION NUMBER: 36,691
;; REFERENCE/DOCKET NUMBER: 1019.3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-496-2300
;; TELEFAX: 415-424-0832
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-383-474B-10

Query Match 70.2%; Score 87; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e-07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FEWTPYQWQPYALPL 21
||||| |||||||||
Db 1 FEWTPGYWQPYALPL 15

RESULT 12
US-08-465-391A-331
; Sequence 331, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/190,788
;; FILING DATE: 02-FEB-1994
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5786331viel, Vern
;; REGISTRATION NUMBER: 32,483
;; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 331:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-465-391A-331

Query Match 70.2%; Score 87; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e-07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FEWTPYQWQPYALPL 21
||||| |||||||||
Db 1 FEWTPGYWQPYALPL 15

RESULT 13
US-08-464-538B-329
; Sequence 329, Application US/08464538B
; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,538B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528A-001810

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 329:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-538B-329

Query Match 70.2%; Score 87; DB 2; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e-07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FEWTPYQWQYALPL 21
||||| |||||||
1 FEWTPGYWQYALPL 15

RESULT 14
US-08-463-076E-12
Sequence 12, Application US/08463076E
Patent No. 5880096
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 392
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,076E
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Snyder, Joseph R.
REGISTRATION NUMBER: 39,381
REFERENCE/DOCKET NUMBER: 16528A-001850US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-076E-12

Query Match 70.2%; Score 87; DB 2; Length 15;
Best Local Similarity 93.3%; Pred. No. 3.3e-07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FEWTPYQWQYALPL 21
||||| |||||||
Db 1 FEWTPGYWQYALPL 15

RESULT 15
US-08-383-474B-300
Sequence 300, Application US/08383474B
Patent No. 5767234
GENERAL INFORMATION:
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Barrett, Ronald W.
APPLICANT: Baldwin, David N.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: the IL-1 Receptor
NUMBER OF SEQUENCES: 314
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend & Townsend & Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,474B
FILING DATE: 01-FEB-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 300:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 17
OTHER INFORMATION: /note= "C-terminal Asp is amidated."
US-08-383-474B-300

Query Match 70.2%; Score 87; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 3.9e-07;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FEWTPYQWQYALPL 21
||||| |||||||
Db 1 FEWTPGYWQYALPL 15

Search completed: August 16, 2001, 14:54:09
Job time: 20 sec

